

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 04-25-02
Searcher: Boyle, E 4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other SCW

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 27, 2002, 18:41:36 : Search time 2503.4 seconds
(without alignments)
8215.445 Million cell updates/sec

Title: US-09-115-660-1

Percent score: 98.1
Sequence: 1 TGGCGCGCAGCTTTTGCAT.....AAAAAAAAAAAAAAAAAAAA 984

Scoring table:
IDENTITY/MQC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 457412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: qb_dai:*
2: qb_dai:*
3: qb_dai:*
4: qb_dai:*
5: qb_dai:*
6: qb_dai:*
7: qb_dai:*
8: qb_dai:*
9: qb_dai:*
10: qb_dai:*
11: qb_dai:*
12: qb_dai:*
13: qb_dai:*
14: qb_dai:*
15: qb_dai:*
16: qb_dai:*
17: qb_dai:*
18: qb_dai:*
19: qb_dai:*
20: qb_dai:*
21: qb_dai:*
22: qb_dai:*
23: qb_dai:*
24: qb_dai:*
25: qb_dai:*
26: qb_dai:*
27: qb_dai:*
28: qb_dai:*
29: qb_dai:*
30: qb_dai:*
31: qb_dai:*
32: qb_dai:*
33: qb_dai:*

Prod. No. is the number of results predicted by chance. have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Score Match Length DB ID Description

1	983	100.0	983	6	AR044575	AR044575	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
2	983	100.0	983	6	AR157660	AR157660	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
3	845.2	86.0	2460	6	AX244978	AX244978	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
4	585	59.5	586	6	AX244978	AX244978	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
5	244.6	24.8	786	8	H024191	H024191	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
6	240.6	24.5	1039	8	H1X111	H1X111	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
7	239	24.3	1123	6	B0006885	B0006885	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
8	239	24.3	1123	6	B0006885	B0006885	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
9	214.6	21.8	2202	8	AF246430	AF246430	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
10	214.4	21.8	928	8	TV1012718	TV1012718	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
11	205	20.9	1195	6	E28866	E28866	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
12	205	20.9	1195	6	E28866	E28866	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
13	203.4	20.7	576	6	SC1292417	SC1292417	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
14	203.4	20.7	2206	8	CEMKB2	CEMKB2	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
15	202.2	20.4	40476	1	SC1756	SC1756	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
16	200.2	20.4	1624	8	APB140X1	APB140X1	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
17	199.8	20.4	1767	1	SHX11	SHX11	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
18	199.6	20.3	851	6	AR2443	AR2443	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
19	199.6	20.3	1640	8	STMX1NB	STMX1NB	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
20	199.4	20.3	1640	8	STMX1NB	STMX1NB	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
21	199.2	20.3	1008	1	AF194025	AF194025	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
22	199.2	20.3	1268	1	085897	085897	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
23	194.8	19.8	2015	8	CEMKA1	CEMKA1	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
24	194.6	19.8	695	8	CNS01CVS	CNS01CVS	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
25	191.6	19.5	1020	9	TRXN1GNA	TRXN1GNA	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
26	190	19.4	1015	6	AR055687	AR055687	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
27	190	19.4	1075	8	567387	567387	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
28	188.2	19.1	514	6	E28872	E28872	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
29	187.8	19.1	2196	1	U01242	U01242	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
30	186.4	19.0	1074	1	AP158618	AP158618	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
31	186	18.9	2009	8	AD003085	AD003085	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
32	185	18.8	1057	6	E02181	E02181	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
33	183.4	18.7	1991	8	HT0238895	HT0238895	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
34	183.4	18.7	1057	6	E02180	E02180	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
35	181.8	18.5	1281	6	AR149835	AR149835	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
36	179	18.2	1080	1	SSX1NG	SSX1NG	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
37	171.8	17.5	572	6	A22913	A22913	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
38	171.6	17.5	617	12	SYNXY1AN	SYNXY1AN	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
39	170.2	17.3	1579	1	AP120156	AP120156	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
40	168.4	17.1	675	6	A25307	A25307	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
41	168.4	17.1	1008	1	STMX1NG	STMX1NG	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
42	166.4	16.9	37420	1	SC111	SC111	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
43	165.6	16.8	516	6	A22805	A22805	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
44	165.2	16.8	927	6	AR100156	AR100156	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999
45	165.2	16.8	927	6	AR137846	AR137846	Sequence 1 from patent US 5817500.	983 bp	DNA	Linear	Pat 29-SEP-1999

ALIGNMENTS

RESULT 1	AR044575	983 bp	DNA	Linear	Pat 29-SEP-1999
LOCUS	Sequence 1 from patent US 5817500.				
DEFINITION	AR044575				
ACCESSION	AR044575.1	GI:5866040			
VERSION	AR044575.1	GI:5866040			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 983)				
AUTHORS	Hansen, J., Kamp, P., Muller, A., and Koop, J. (1998)				
TITLE	Animal food additives				
JOURNAL	Patent: US 5817500-A 1 05-0CT-1998				
FEATURES	location/qualifiers				
source	1..983				
BASE COUNT	225 a 272 c 277 g 209 t				
ORIGIN					

Query Match 130.0% Score 98.3 OP 6: Length 983
Host Local Similarity 130.0% Prod. No. 1.86-2.41

		/gene="xyna"		/feature="determined by homology"		/product "endo-beta-1,4-D-xylanase"	
polYA-site		2106					
BASE COUNT	615 a	626 c	628 g	591 t			
ORIGIN							
Query Match	86.0% Score 845.2; DB 8; Length 2400						
Best Local Similarity	89.8%; Prod. No. 1.70-1.97						
Matches 953; Conserved type 0; Mismatches 4; Indels 104; Gaps 1							
QY	1	TCGGCCGACGCTCTTCGCATCTCTTCATGATGGGCGGGCTTATCGGCGGCTTGGCGG	60				
DB	1035	TCGGCCGACGCTCTTCGCATCTCTTCATGATGGGCGGGCTTATCGGCGGCTTGGCGG	1094				
QY	61	CGCTTAGCGCGACCTGGGAGCCCTGGCCTTCGCGAGAGAAATCGGAGAGCTGAAAG	120				
DB	1095	CGCTTAGCGCGACCTGGGAGCCCTGGCCTTCGCGAGAGAAATCGGAGAGCTGAAAG	1154				
QY	121	CGACGAAACACTCTGCACCTCGGAGGGCTGGACGATGTTATTAATATCTGATGACT	180				
DB	1155	CGACGAGCAATCTCTCAATTCGGAGGGCTGGACGATGTTATTAATATCTGATGACT	1214				
QY	181	GAGCGCTGCAATCGCAATCGAGCTACACCACTGGAGACCGCGAGCTATCGAATCATGG	240				
DB	1215	GAGCGCTGCAATCGCAATCGAGCTACACCACTGGAGACCGCGAGCTATCGAATCATGG	1274				
QY	241	GGAGATGGAGCTAAATTCGTCGATGGAAAGACCTGCAATCGGAGCTTAAAGCTA	294				
DB	1275	GGAGATGGAGCTAAATTCGTCGATGGAAAGACCTGCAATCGGAGCTTAAAGCTA	1344				
QY	295	-----	294				
DB	1345	GTGTCCCTCAAGATCAATATACCGAATATTAATCGCTTCAATGATGATGATTA	1394				
QY	295	-----	414				
DB	1395	GCTTCTCTTAATCTCAACCACTTAACTAAATCTGTATATGAATAGAAATATATAT	1454				
QY	415	TCCTTATTAATGAAATGCAATGCAAGATTAATCTGCGATCATGATGCAATGCAAT	474				
DB	1455	TCCTTATTAATGAAATGCAATGCAAGATTAATCTGCGATCATGATGCAATGCAAT	1514				
QY	475	GATGCAATGATTAATATGCGCAATATCTGCAATGATGATGATGATGATGATGAT	484				
DB	1515	GATGCAATGATTAATATGCGCAATATCTGCAATGATGATGATGATGATGATGAT	1574				
QY	485	TCATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	494				
DB	1575	TCATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1634				
QY	495	CGACATTAATGAAATGCAATGCAAGATTAATCTGCGATCATGATGCAATGCAAT	554				
DB	1635	CGACATTAATGAAATGCAATGCAAGATTAATCTGCGATCATGATGCAATGCAAT	1694				
QY	555	GGCGCAATGATTAATGCAATGCAAGATTAATCTGCGATCATGATGCAATGCAAT	614				
DB	1695	GGCGCAATGATTAATGCAATGCAAGATTAATCTGCGATCATGATGCAATGCAAT	1754				
QY	615	GAAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	674				
DB	1755	GAAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1814				
QY	675	GTATGTCGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT	734				
DB	1815	GTATGTCGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1874				
QY	735	GGTAAACGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT	794				
DB	1875	GGTAAACGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1934				

[illegible]

Db 235 AGGGTACTCTGCTACTGCTACTGCTAGGATGGCAGGCGGCGGCTGCTAGTAACTATGCTT 234

QY 215 AAGCGCGGCACTACGAGATCACTGAGGAGATGGCGGTAACTGCTGGCTGAGAAAGAT 274

Db 295 GCGCGCGGCACTACGAGATCACTGAGGAGATGGCGGTAACTGCTGGCTGAGAAAGAT 354

QY 275 GCGCGCGGCACTACGAGATCACTGAGGAGATGGCGGTAACTGCTGGCTGAGAAAGAT 334

Db 335 GCGCGCGGCACTACGAGATCACTGAGGAGATGGCGGTAACTGCTGGCTGAGAAAGAT 394

QY 335 AATAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 394

Db 415 AATAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 474

QY 395 AATAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 454

Db 475 GCGCGCGGCACTACGAGATCACTGAGGAGATGGCGGTAACTGCTGGCTGAGAAAGAT 534

QY 455 AATAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514

Db 535 AATAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594

QY 515 GCGCGCGGCACTACGAGATCACTGAGGAGATGGCGGTAACTGCTGGCTGAGAAAGAT 574

Db 595 GCGCGCGGCACTACGAGATCACTGAGGAGATGGCGGTAACTGCTGGCTGAGAAAGAT 654

QY 575 AATAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 634

Db 655 AATAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714

QY 635 AATAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692

Db 712 AATAGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769

RESULT 6

LOCUS HXXYL 1039 bp mRNA linear PCN 10-FEB-1999

DEFINITION HXXYL mRNA for endoglucanase.

ACCESSION X76047.1 GI:505240

VERSION X76047.1 GI:505240

KEYWORDS endoglucanase; xyl1 gene.

SOURCE Humicola insolens.

ORGANISM Humicola insolens

REFERENCE 1 (bases 1 to 1039)

AUTHORS Dalgaard, H.

TITLE Direct Substitution

JOURNAL Submitted (04-NOV-1993) H. Dalgaard, Manager, Genetec, Novo Nordisk A/S, Symion, (Friedbergvej) 3, 2100 Copenhagen, DK, DENMARK

REFERENCE 2 (bases 1 to 1039)

AUTHORS Dalgaard, H. and Heldt-Hansen, H. P.

TITLE A novel method for efficient expression cloning of fungal enzyme genes

JOURNAL Mol. Gen. Genet. 243 (3), 253-260 (1994)

FEATURES

source location/qualifiers

1..1039

/organism "Humicola insolens"

/db_xref "taxon:34413"

sig_peptide 47..103

gene "XYL1"

47..730

/gene "XYL1"

47..730

/gene "XYL1"

/ec_number "3.2.1.8"

/product "endo-1,4-beta-xylanase"

/protein_id "CAA54632.1"

/db_xref "GI:505240"

/db_xref "SWISS Prot:P55334"

/translation "MVALSKVLAAMAVASSAIADPDEVPENSTALCAQVYTNAAE"

WINGFYSSWISGSGGQVYTNLESPYVRRRTDNFVGRKMNIGPNTNAYFN
PUGKGLAVYQMTNPDLVETVETSTYNGSALVKGLEYTGVYVSVRNG
PSIDGRTEDYVWISIRKRRVGGVNMNHNAMQJHOMLQJHYVAVVAVYSSG
ESDIYVQIH"

BASE COUNT 218 a 425 c 273 g 223 t

ORIGIN

Query Match 24.5% Score 240.6 E-49 H: Length 1039

Best Local Similarity 64.6% Prod. No. 1.2e-48

Matches 392 Conserved 0 Mismatches 209 Indels 6 Gaps 2

QY 87 CTTCGGGAGAGAAATGACGAGATGAAAGGAGAAATGAAATGAAATGAAATGAAATGAAAT 146

Db 118 CTTTCGGGAGAGAAATGACGAGATGAAAGGAGAAATGAAATGAAATGAAATGAAATGAAAT 177

QY 147 CTGGGAG 206

Db 178 CTGGGAG 247

QY 207 CAAGCTGAG 266

Db 248 CAAGCTGAG 297

QY 267 AAG 326

Db 298 AAG 354

QY 327 AAG 386

Db 355 AAG 414

QY 387 CATCTGAG 446

Db 415 CATCTGAG 474

QY 447 CATCTGAG 506

Db 475 CATCTGAG 534

QY 507 CATCTGAG 566

Db 535 CATCTGAG 594

QY 567 TACGCTGAG 626

Db 595 TACGCTGAG 654

QY 627 TACGCTGAG 686

Db 652 TACGCTGAG 714

QY 687 TACGCTGAG 714

Db 712 TACGCTGAG 769

RESULT 7

LOCUS BD006885 1123 bp DNA linear PAT 31-JAN-2002

DEFINITION Aspergillus expression system.

ACCESSION BD006885

VERSION BD006885.1 GI:18645256

KEYWORDS JP 2001025493-A/2.

SOURCE Humicola insolens.

ORGANISM Humicola insolens

REFERENCE 1 (bases 1 to 1123)

AUTHORS Becker, R.M., Godoy, W., Takai, S. and Hoshino, Y.

TITLE Aspergillus expression system

JOURNAL Patent JP 2001025493-A 2 30-JAN-2001

COMMENT

OS Humicola insolens

[illegible][illegible]

COMMENT US Streptomyces olivaceoviridis
 PN JP 1998090702
 PE 05-00T-1998
 PR 20-MAR-1998 JP 1998090702

PI SATOSHI KANEKO, KIYOSHI HAYASHI
 PC G12N15/09, G12N1/21, G12N9/26// (G12N15/09, G12N1/465), (G12N1/21,
 PG G12N1/19)
 PC G12N15/09, (G12N15/09, G12N1/465)
 CC Strandness: double;
 CC Topology: linear;
 PH Key Location/Qualifiers
 FT map peptide 418..993
 Location/Qualifiers
 source 1..1195
 /organism="Streptomyces olivaceoviridis"
 /db_xref="taxon:32844"

BASE COUNT 230 a 457 c 333 q 175 t
 ORIGIN

Query Match 20.7%; Score 205; DB 6; Length 1195;
 Best Local Similarity 62.7%; Pred. No. 7, 1e-40;
 Matches 354; Conservative 0; Mismatches 200; Indels 9; Gaps 2;

QY 130 ACCGCCACTGCGAGGCGTGGCAGATGTTATTCATTCTGTCGATCTATCTGCA 189
 III IIII I III IIII IIII IIII IIII IIII IIII IIII IIII IIII
 DB 430 ACCGACACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 489
 QY 190 GCGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249
 I
 DB 490 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
 I
 QY 250 GGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309
 I
 DB 550 GGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609
 I
 QY 310 GAGGCTGTTACGACGCGAAGGCGACGACGACGACGACGACGACGACGACG 369
 I
 DB 607 TCGGCGACGCTTTCGACGCTTTCGACGCTTTCGACGCTTTCGACGCTTTCG 666
 QY 370 CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429
 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
 DB 667 CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 QY 430 ACCGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 489
 I
 DB 721 ACCGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
 QY 490 GTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
 I
 DB 781 TATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 550 GATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609
 I
 DB 841 TCGGCGACGCTTTCGACGCTTTCGACGCTTTCGACGCTTTCGACGCTTTCG 900
 QY 610 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669
 I
 DB 901 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 670 AGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692
 IIII IIII I I I I I I
 DB 961 AGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 983
 RESULT 13
 SOL292417 576 bp DNA linear FCT 21-DEC-2000
 LAMOS Streptomyces olivaceoviridis partial xylnl gene for beta-xylanase.
 DEFINITION AJ292417.1 G1-11967886
 ACCESSION
 VERSION
 KEYWORDS beta-xylanase; xylnl gene.

SOURCE Streptomyces olivaceoviridis.
 ORGANISM Streptomyces olivaceoviridis
 Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
 Actinomycetales; Streptomyces; Streptomyces; Streptomyces.
 REFERENCE 1 (bases 1 to 576)
 AUTHORS Zhang, H., Yao, B. and Wang, Y.
 TITLE Cloning and expression of the 23kD beta-xylanase gene from Streptomyces olivaceoviridis R-86
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 576)
 AUTHORS Bin, Y.
 TITLE Direct Submission
 JOURNAL Submitted (20-DEC-2000) Bin Y, Chinese Academy of Agricultural Sciences, Food Research Institute, 12 Zhongguancun Road, Beijing, 100081, CHINA
 FEATURES
 source 1..576
 /organism="Streptomyces olivaceoviridis"
 /strain="E-86"
 /db_xref="taxon:1921"
 /country="Japan"
 1..576
 /gene="xylnl"
 <1..576
 /feature="xylnl"
 /EC_number="3.2.1.8"
 /function="Hydrolase xylan"
 /codon_start=1
 /transl_table=1
 /product="beta-xylanase"
 /protein_id="CAC19491.1"
 /db_xref="GI:11967887"
 /translation="ATVITNQTCTNNGYSEWIDGGSMTLNSGNYSTWTN"
 GNEPAAGKSMGRNVOYSGSEFSGKYLALGWSIINLVEVYIVNMGKPLGT
 YKGYISGGTYDYUTRYNAPSVSEKTNQVWSYKSRIGGIIITSHHDMAAR
 YGMOLGSHYMIILATEBYGSSGSLTVSC"

BASE COUNT 125 a 208 c 164 g 79 t
 ORIGIN

Query Match 20.7%; Score 203.4; DB 1; Length 576;
 Best Local Similarity 62.7%; Pred. No. 1, 6e-39;
 Matches 353; Conservative 0; Mismatches 201; Indels 9; Gaps 2;

QY 130 ACCGCCACTGCGAGGCGTGGCAGATGTTATTCATTCTGTCGATCTATCTGCA 189
 III IIII I III IIII IIII IIII IIII IIII IIII IIII IIII IIII
 DB 13 ACCGACACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 72
 QY 190 GCGGAGGCGACGATGACGACGATGACGACGATGACGACGATGACGACGATGAC 249
 I
 DB 73 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 79
 QY 250 GGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309
 I
 DB 133 GGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 189
 QY 310 GAGGCTGTTACGACGCGAAGGCGACGACGACGACGACGACGACGACGACG 369
 I
 DB 190 TCGGCGACGCTTTCGACGCTTTCGACGCTTTCGACGCTTTCGACGCTTTCG 249
 QY 370 CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429
 IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
 DB 250 CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303
 QY 430 ACCGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 489
 I
 DB 304 ACCGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 363
 QY 490 GTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
 IIII IIII
 DB 364 TACGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423
 QY 550 GACGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609

424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815																																																																																																																																																																																									

[illegible]

REFERENCE 1 (bases 1 to 40476)
 Redenbach, H., Kleser, H.M., Denapite, D., Eichner, A., Cullum, J., Kinsahl, M., and Hopwood, D.A.
 A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A1(2) chromosome
 Mol. Microbiol. 21 (1), 77-96 (1996)

JOURNAL MEDLINE
 2 (bases 1 to 40476)
 Seeger, K.J., and Harris, D.
 Unpublished
 3 (bases 1 to 40476)
 Thomson, N.R., Parkhill, J., Barrell, B.G., and Rajandream, M.A.
 Direct Submission
 Submitted (01-DEC-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [1] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK

COMMENT
 Streptomyces coelicolor sequencing at The Sanger Centre is funded by the HHSKJ and Wellcome Genomics
 Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
 (URL: <http://www.sanger.ac.uk/projects/S-coelicolor/>)
 CDS are numbered using the following system: sc787.01c, SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary strand).
 The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
 The length in codons is given for each CDS.
 Usually the highest scoring match found by fasta is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
 Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krohn et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at <http://www.uh.ro.jp/jm/Gen-Bin/FramePlot.pl>. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
 cosmid C75A overlaps with cosmid 152 and C30 on the AseI-C genomic restriction fragment.

FEATURES
 source location/Qualifiers
 1..40476
 /organism "Streptomyces coelicolor A1(2)"
 /strain "A1(2)"
 /db_xref "taxon:100226"
 /clone "cosmid C75A"
 1..102
 /note "nominal overlap with cosmid S1162"
 /complement(1..804)
 /note "sc75A.01c"
 /note "sc75A.01c, possible membrane protein, partial CDS, len > 268 aa. Highly similar to another putative membrane protein from Streptomyces coelicolor
 TR:CA845491(EMBL:AL079348) SC6613.03 (330 aa), fasta scores opt: 695 z-score: 823.4 E(-0.54, 0.88 identity in 241 aa overlap, contains possible membrane spanning hydrophobic domains."
 /codon_start 1
 /transl_table 11
 /product "putative membrane protein."

CDS
 misc_feature
 CDS

gene
 RBS
 RBS
 gene
 CDS

/protein_id="CA861701.1"
 /db_xref="GI:6469240"
 /translation="MAQAVMTETDGGSDPERRENRIRLPDRAVGMKDIRIMWRGLTAFAVALLSLMAASHSTIPNATGSLITETPIWHQGLIPVLLVIAVLSKATAALIAVYVSWYMLPGGLIPDRKSGSDITVARNVANNADQVATARRAAAGAVMATEIKASAVPTYEKALAAKPRHAYVGVYGLSKRPVTSVKVCTIEIEMKRAMRATVTSVGPVAVVAHPSYKRLKAFPTARQKSAIMAGVISHKRPK1"
 /complement(1..804)
 /gene="sc75A.01c"
 /complement(812..815)
 1110..1115
 1124..1199
 /gene="panb"
 1124..1199
 /note="panb"
 /note="sc75A.02, panb, 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11), len: 291 aa. Highly similar to many including: Escherichia coli SW:PANB_ECOLI(EMBL:D17086) 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) (264 aa), fasta scores opt: 711 z-score: 839.4 E(-0.44, 0.88 identity in 262 aa overlap and Mycobacterium tuberculosis SW:PANB_MYCTI(EMBL:D70692) 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) (281 aa), fasta scores opt: 1019 z-score: 1199.2 E(-0.59, 1.88 identity in 269 aa overlap."
 /codon_start 1
 /transl_table 11
 /product="3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)."
 /protein_id="CA861702.1"
 /db_xref="GI:6469241"
 /translation="MTOLSAQTTPUPKADGNRAIVYGRKINRITVHDIYAAEKCKWPMITADAMTASVDFSGIPVMVVDSDGNCNHLGFTTVPVTLIDETIMLSAAYVKIISRAIIVDDLFEGSYGEGVQALRSATIMVEACVAGAKLEGSRSHQLEILVSGIPVMAHIGLITPSVNSMGVRYGGRGHEAGQILRDRAKVDGAPAVVEIYEPALAEVTRLIHTVIGAGPOTDAQVLTWITMIGITGSRMRKFGVGYMLRKVMIAKAAVADVVGITPADHSYH"
 2119..3216
 /gene="sc75A.03"
 /note="sc75A.03"
 /note="sc75A.03, probable ARC transporter, ATP-binding component, len: 365 aa. Highly similar to many ARC transport proteins e.g. Streptomyces punctatus SW:DRKA_STRPT(EMBL:M73758) dantrolone resistance ATP-binding protein (330 aa), fasta scores opt: 922 z-score: 1009.0 E(-0.48, 0.94 identity in 329 aa overlap and Streptomyces antibioticus TR:Q53116(EMBL:L06249) ATP-binding protein ORF-0884 involved in olendomycin resistance (325 aa), fasta scores opt: 1883 z-score: 2052.8 E(-0.89, 0.78 identity in 329 aa overlap. Also similar to several Streptomyces coelicolor putative ARC transporters ATP-binding components e.g. TR:CA842771(EMBL:AL049841) SC69.25 (315 aa), fasta scores opt: 1031 z-score: 1127.7 E(-0.54, 0.88 identity in 318 aa overlap, contains positive hits to conserved ATP-binding site motif A (P-loop) and P080211 ARC transporters family signature. Also contains a P-loop match to entry P080005 ARC_tran, ARC transporter."
 /codon_start 1
 /transl_table 11
 /product="probable ARC transporter, ATP-binding component."
 /protein_id="CA861703.1"
 /db_xref="GI:6469242"
 /translation="MAVAGRWGVGALSVPPAVYWRKRLIDIPRAASAVYKGLVHYGTRKALDSDVLDVIRGVGVGIPGAGKTLVLPILSTLITPISGCAVAVYVVRQKPLRSVIGITGVYASVDPKIPQEWYIMIGRLIDISPAKATKACVILLERSTEEAGKPRASYSGMRRLDASMSGHPVLLPDLPIIDIDRIENKAWYKRWYGVVTVLLITGYMEAGHJASLTIVYDGRKATIEIKAKVGCITLIRANLQDHLAAVDELGTGJASVSTYRKGTIVLVLTISDQITAVAGAVAKNIVASVITLHSLDENVLTIGKASAVQDPATVTDITRELVAV"
 2119..3216

[illegible][illegible][illegible][illegible]

Protein "secretase A," probably A α 1 and A α 2, is a component, pI = 274. Similar to many transport proteins

SW: DREX SLRFE(EMOL:M73758) dannonobiofin poststidnoce
4 tsonembarane ptoofin (283 45) lasta sctozes opt: 622
t sonembarane ptoofin (283 45) lasta sctozes opt: 245 44

oxovalap and streptomycins and their analogs, Trg55717 (IMC-10624) membrane protein of 537 aa, involved in colicinogenicity in *Escherichia coli*. It has a structure of 2

hydropathic domains."

$$\frac{\text{Transportable}}{\text{product}} = \frac{\text{probable ABC transporters}}{\text{transporters}}$$

/proc/101104.1
 /lib/xrt/101:669243
 /lib/xrt/101:MSAATYAPPTLETHOAKTIPRAHRIHSAIIRNLIWIRIOPPS
 /lib/xrt/101:MSAATYAPPTLETHOAKTIPRAHRIHSAIIRNLIWIRIOPPS

[illegible]

Geometry	2D, 3D	Stress, 2D, 3D	14.6, 16
Material	50, 100	Prod. No. 4, 80, 99	
Simulation			

[illegible][illegible][illegible]

40146 CAGTGGTATGCTGCTATGACATGCGGTTCCGCGCGCTACTACAGAGACCTTCTGTGTTGTTAAAG 40087

[illegible][illegible][illegible]

89909 2A87C2717C1032AC21A67A1E7C7E72AC2A867B6D0D5267A7C9312B793A87E227C
89910

[illegible][illegible][illegible][illegible]

667 AACAAACATTAAGCTTGTATTATGTTCTAATACTGGTAACCTGAATCTC / 19
|||||

DOI: 10.1002/anie.201500075

Search completed: April 27, 2002, 19:59:29
Job time: 4673 sec

CC a plasmid pYES2.0 vector in *Saccharomyces cerevisiae* DSM 10153
 CC (clonimex), and may be added to flour at 5-5,000 (preferably 20-2,000)
 CC FXU/kg flour, optionally along with other enzymes (amylase,
 CC maltogenase, lipase, cellulase, hemicellulase, pentosanase, glucose-
 CC oxidase, lactase, protease and/or peroxidase). The enzyme combines
 CC particularly well with amylolytic enzymes, and may be used to
 CC improve baking properties of flour and/or dough, by increasing
 CC volume and improving texture, flavour, crumb softness, freshness
 CC and anti-staling properties, while improving dough machinability
 CC and stability.
 CC
 XX
 XX Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 other;

Query Match 100.0%; Score 983; DB 17; Length 984;
 Best Local Similarity 100.0%; Pred. No. 4,56-256;
 Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGCGGACGCTTTCGATCCTTGCATGATGCTGGCTTACCGCGGAGCTTTCG 60
 DB 1 TCGGCGGACGCTTTCGATCCTTGCATGATGCTGGCTTACCGCGGAGCTTTCG 60
 QY 61 GCTTACCGCGGACGCTTTCGATCCTTGCATGATGCTGGCTTACCGCGGAGCTTTCG 120
 DB 61 GCTTACCGCGGACGCTTTCGATCCTTGCATGATGCTGGCTTACCGCGGAGCTTTCG 120
 QY 121 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 180
 DB 121 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 180
 QY 181 GACGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 240
 DB 181 GACGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 240
 QY 241 GACGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
 DB 241 GACGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
 QY 301 ATCCGCTTTCGAGGCTTTACGACGACGACGACGACGACGACGACGACGACGACGACG 360
 DB 301 ATCCGCTTTCGAGGCTTTACGACGACGACGACGACGACGACGACGACGACGACGACG 360
 QY 361 ATCCGCTTTCGAGGCTTTACGACGACGACGACGACGACGACGACGACGACGACGACG 420
 DB 361 ATCCGCTTTCGAGGCTTTACGACGACGACGACGACGACGACGACGACGACGACGACG 420
 QY 421 TCGGCGGACGCTTTCGATCCTTGCATGATGCTGGCTTACCGCGGAGCTTTCG 480
 DB 421 TCGGCGGACGCTTTCGATCCTTGCATGATGCTGGCTTACCGCGGAGCTTTCG 480
 QY 481 ACCGCTTTCGAGGCTTTACGACGACGACGACGACGACGACGACGACGACGACGACG 540
 DB 481 ACCGCTTTCGAGGCTTTACGACGACGACGACGACGACGACGACGACGACGACGACG 540
 QY 541 GTCCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 600
 DB 541 GTCCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 600
 QY 601 GTCCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 660
 DB 601 GTCCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 660
 QY 661 TACTGATCTTCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 720
 DB 661 TACTGATCTTCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 720
 QY 721 TACTGATCTTCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 780
 DB 721 TACTGATCTTCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 780
 QY 781 ATACGATATCTTCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 840
 DB 781 ATACGATATCTTCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 840

QY 841 GAGCTTTCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 900
 DB 841 GAGCTTTCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 900
 QY 901 TACTGATCTTCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 960
 DB 901 TACTGATCTTCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 960
 QY 961 AAAAAAAAAAAAAAAAAAAAAA 983
 DB 961 AAAAAAAAAAAAAAAAAAAAAA 983

RESULT 3

AA513813
 ID AA513813 standard; DNA; 588 BP.

AC AA513813;

DE 18-DEC-2001 (first entry)

DE DNA encoding *Thermomyces lanuginosus* xylanase A.

KM Xylanase A: plant cell wall; baking; cereals; starch production; wood;
 KM wood pulp bleaching; hemicellulose; arabinoxylan; foodstuffs; bread; etc.

XX *Thermomyces lanuginosus*.

XX W0200167711-A1.

XX 13-SEP-2001.

XX 08-MAR-2001; 2001W0-1B00426.

XX 08-MAR-2001; 2000G0-0005585.

XX 27-JUN-2000; 2000G0-0015751.

XX (DANI-) DANISCO AS.

XX Sildesen O. Sorensen JF;

XX WPI: 2001-546844/67.

XX Novel variant xylanase polypeptide or its fragment useful for degrading
 XX or modifying plant cell wall, comprises amino acid modifications such
 XX that the polypeptide has altered sensitivity to xylanase inhibitor

XX Disclosure: Page 64; 70pp; English.

XX The invention relates to a variant xylanase polypeptide (I) or its
 XX fragment having xylanase activity, comprising one or more amino acid
 XX modifications such that (I) or its fragment has an altered sensitivity to
 XX a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or
 XX its coding sequence (II) is useful for degrading or modifying plant cell
 XX wall or for processing a plant material by contacting the plant cell wall
 XX or plant material with (I) or (II). (I) is useful for modifying plant
 XX materials, and in baking, processing cereals, starch production,
 XX processing wood and enhancing the bleaching of wood pulp. (I)
 XX is useful for altering the viscosity derived from the presence of
 XX hemicellulose or arabinoxylan in a solution or system comprising plant
 XX cell wall material. (I) is useful for preparing a foodstuff such as
 XX bread, pretzels, tortillas, cakes, cookies, biscuits or crackers.
 XX The present sequence represents the coding sequence of *Thermomyces*
 XX *lanuginosus* xylanase A as described in the method of the invention

XX Sequence 588 BP; 131 A; 178 C; 168 G; 111 T; 0 other;

Query Match 59.5%; Score 585; DB 22; Length 588;
 Best Local Similarity 100.0%; Pred. No. 1,90-148;
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible][illegible]

[illegible]

Search completed: April 27, 2002, 21:07:49
Job time: 8588 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 27, 2002, 18:42:36 : Search time 65.8 seconds
(without alignments)
3669,570 Million cell updates/sec

Title: US-09-115-660-1
Sequence: 1 TCGGCTTCGAGCTTTCGAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY_MQC
Gapop 10.0, Gapext 1.0

Search: 48353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents,NA.*
1: /cpn2_6/ptdata/1/ina/5A_COMB.seq:*
2: /cpn2_6/ptdata/1/ina/5B_COMB.seq:*
3: /cpn2_6/ptdata/1/ina/6A_COMB.seq:*
4: /cpn2_6/ptdata/1/ina/6B_COMB.seq:*
5: /cpn2_6/ptdata/1/ina/PCIDS_COMB.seq:*
6: /cpn2_6/ptdata/1/ina/backlist1.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the result total printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	983	100.0	983	1	US-08-886-765-1
2	983	100.0	983	4	US-09-115-660-1
3	249	24.3	1123	1	US-08-458-023B-3
4	197.2	20.1	1375	2	US-08-468-812-1
5	197.2	20.1	1375	4	US-08-590-563-1
6	194.2	19.8	822	4	US-09-254-733-8
7	190	19.3	1015	2	US-08-121-436A-1
8	181.8	18.5	1281	4	US-08-766-373-1
9	168.4	17.1	675	1	US-07-744-570B-1
10	165.2	16.8	927	1	US-08-507-431-5
11	165.2	16.8	927	2	US-08-902-655A-5
12	165.2	16.8	927	4	US-09-116-622-5
13	165.2	16.8	927	4	US-09-219-277-5
14	165.2	16.8	927	4	US-09-599-661-5
15	162.4	16.5	489	1	US-08-119-169A-7
16	159	16.2	2219	1	US-08-290-979A-7
17	144.8	14.7	573	1	US-08-709-912-18
18	144.8	14.7	573	2	US-09-047-370-18
19	138	14.0	1174	4	US-08-768-373-3
20	119	12.1	744	4	US-09-189-060B-11
21	108.8	11.1	1207	1	US-08-575-564-2
22	108.8	11.1	1207	2	US-08-963-500-2
23	103.6	10.5	2054	4	US-08-981-724-5
24	98.2	10.0	2059	1	US-08-244-686-1
25	97.6	9.9	954	1	US-08-315-695-15
26	96.2	9.8	234	4	US-09-189-060B-46
27	95.8	9.7	847	4	US-09-260-283-1

28	94	9.6	2055	1	US-07-842-349-1	Sequence 1, Appl 1
29	84.6	8.6	941	2	US-08-121-436A-3	Sequence 4, Appl 1
30	82.6	8.4	642	1	US-08-104-445-2	Sequence 2, Appl 1
31	82.6	8.4	1413	1	US-08-104-445-1	Sequence 1, Appl 1
32	82.2	8.4	579	1	US-08-709-912-19	Sequence 19, Appl 1
33	82.2	8.4	579	2	US-09-047-370-19	Sequence 39, Appl 1
34	81	8.2	572	1	US-08-044-6210-3	Sequence 5, Appl 1
35	80.8	8.2	1142	4	US-08-768-473-5	Sequence 47, Appl 1
36	77.4	7.9	234	4	US-09-189-060B-47	Sequence 46, Appl 1
37	77.2	7.9	234	4	US-09-189-060B-48	Sequence 12, Appl 1
38	76.6	7.6	1244	3	US-08-591-685-12	Sequence 1, Appl 1
39	74.2	7.5	744	4	US-09-189-060B-1	Sequence 1, Appl 1
40	74.2	7.5	871	1	US-08-698-978-1	Sequence 1, Appl 1
41	72.6	7.4	744	4	US-08-501-126-18	Sequence 18, Appl 1
42	72.4	7.4	663	4	US-08-470-954A-1	Sequence 1, Appl 1
43	72.4	7.4	663	4	US-08-470-954A-2	Sequence 2, Appl 1
44	72.4	7.4	744	4	US-08-470-954A-4	Sequence 4, Appl 1
45	72.4	7.4	744	4	US-08-470-954A-5	Sequence 5, Appl 1

ALIGNMENTS

RESULT 1
US-08-886-765-1
Sequence 1, Application US/08886765
Patent No. 5817500
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Mullertz, Anette
APPLICANT: Knapp, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: No 58175000 No. 5817500disk of No. 5817500th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lamberts, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Thermomyces lanuginosus
STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705
US-08-886-765-1

QY 241 GAGATGGCGGTAACTGCTGCTGGAAGGCTGGAACCCGAGCTGAACTGAAGACT 300
 DB 241 GAGATGGCGGTAACTGCTGCTGGAAGGCTGGAACCCGAGCTGGAAGACT 300
 QY 301 ATGCACTTGAAGGCTTACAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG 400
 DB 301 ATGCACTTGAAGGCTTACAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG 400
 QY 361 ACCGCGCAACCGCTGCTGCAATTAACATGCTGGAACCTTGGAGCTGCTGCT 420
 DB 361 ACCGCGCAACCGCTGCTGCAATTAACATGCTGGAACCTTGGAGCTGCTGCT 420
 QY 421 TCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 DB 421 TCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 481 AGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 DB 481 AGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 541 GTCGCGCAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG 600
 DB 541 GTCGCGCAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG 600
 QY 601 GCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 601 GCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 661 TACTTGAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG 720
 DB 661 TACTTGAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG 720
 QY 721 TGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 DB 721 TGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 781 ATGCACTTGAAGGCTTACAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG 840
 DB 781 ATGCACTTGAAGGCTTACAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG 840
 QY 841 GAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 DB 841 GAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 QY 901 TGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 901 TGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 961 AAAAAAAAAAAAAAAAAAAAAA 983
 DB 961 AAAAAAAAAAAAAAAAAAAAAA 983
 RESULT 3
 ? Sequence 3, Application US/08458023B
 ? GENERAL INFORMATION:
 ? PATENT No. 5667990
 ? APPLICANT: Hoeke, Randy M.
 ? APPLICANT: Yoder, Wendy
 ? APPLICANT: Lakadi, Shindhu
 ? APPLICANT: Karamathu, Karuppan C.
 ? TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
 ? NUMBER OF SEQUENCES: 16
 ? CORRESPONDENT'S ADDRESS:
 ? ADDRESSEE: No. 5667990 No. 5667990disk of No. 5667990th America, Inc.
 ? STREET: 405 Lexington Avenue
 ? CITY: New York
 ? STATE: New York
 ? COUNTRY: USA
 ? ZIP: 10174-6201
 ? COMPUTER REIMAHLE FORM:
 ? MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/458,023B
 ? FILING DATE: 01-JUN-1995
 ? CLASSIFICATION: 435
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Lowrey Jr., Karen A.
 ? REGISTRATION NUMBER: 41,274
 ? REFERENCE/FILE NUMBER: 4086,010-US
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 212-867-0123
 ? TELEFAX: 212-878-9655
 ? INFORMATION FOR SEQ ID NO: 3:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1123 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (genomic)
 ? HYPOTHEetical: NO
 ? ANTI-SENSE: NO
 ? FRAGMENT TYPE: Internal
 ? ORIGINAL SOURCE:
 ? ORGANISM: Humicola insolens
 ? INDIVIDUAL ISOLATE: DSM 6495
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: 126..806
 ? US-08 458-023B-1
 Query Match 24.3% Score 239; DB 1; Length 1123;
 Best local similarity 64.4%; Pred. No. 1,80-58;
 Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;
 QY 87 CTTCGCGAGAGATATGCGAGAGCTGCAAAAGGCAAGAGCAAGAGCAAG 146
 DB 197 GTTCTGCGAGAGATATGCGAGAGCTGCAAAAGGCAAGAGCAAGAGCAAG 256
 QY 147 CTTCGCGAGAGATATGCGAGAGCTGCAAAAGGCAAGAGCAAGAGCAAG 206
 DB 257 CTTCGCGAGAGATATGCGAGAGCTGCAAAAGGCAAGAGCAAGAGCAAG 416
 QY 207 GAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266
 DB 417 GAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
 QY 267 AAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
 DB 377 AAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
 QY 327 AAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386
 DB 434 GAGGCGAGAGAGTACCTGCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 496
 QY 387 GAGGCGAGAGAGTACCTGCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 446
 DB 494 TGTGAGGAGAGTACCTGCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 556
 QY 447 GAGGCGAGAGAGTACCTGCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 506
 DB 554 GAGGCGAGAGAGTACCTGCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 616
 QY 507 GAGGCGAGAGAGTACCTGCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 566
 DB 614 GAGGCGAGAGAGTACCTGCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 676
 QY 567 TACGCTGAGAGAGTACCTGCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 626
 DB 674 CTGCTGAGAGAGTACCTGCGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 740


```

? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.10
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/590,563
? FILING DATE: 26-JAN-1996
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/468,812
? FILING DATE: 06-JUN-1995
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/332,412
? FILING DATE: 31-OCT-1994
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/282,001
? FILING DATE: 29-JUL-1994
? CLASSIFICATION: 536
? ATTORNEY/AGENT INFORMATION:
? NAME: Rudalsky, Lawrence B.
? REGISTRATION NUMBER: 35,086
? REFERENCE/DOCKET NUMBER: 1050.034003
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-371-2600
? TELEFAX: 202-371-2540
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1375 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: not relevant
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 303..1334
? US-08-590-563-1

```

Query Match 20.1% Score 197.2; DB 4; Length 1375;
 Best Local Similarity 58.6%; Pred. No. 1,40-46;
 Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;

```

QY 35 TCGATTACCGCGGCTGCTGGTGGGCTTACCGCGGATGCGGCTGGCTTTCGGG 94
DB 349 TCGGCTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 408
QY 95 CAGCGAATGCGCAGGAGCTGCAAAAGCAGACAGAAACGCAATTCGAGCTGCTGCTG 134
DB 409 TCTGCGCGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
QY 155 ATGCTATTACTATTCCTGCTGAGTGAAGGCTGAGAGCTGAGAGCTGAGAGCTG 214
DB 469 ACGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
QY 215 AAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 274
DB 529 CGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
QY 275 GGAACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 334
DB 589 GGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
QY 335 ACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 394
DB 646 ACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
QY 395 AGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 454
DB 706 ACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
QY 455 ACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
DB 760 ACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819

```

```

QY 515 CCCAAACCTTCGACCAATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574
DB 820 CCGGACGCTTCAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 879
QY 575 AGACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 644
DB 880 CCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 946
QY 635 ACTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 994
DB 937 ACTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 996
QY 695 CTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722
DB 997 GCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1024

```

RESULT 6
 US-09-254-733-8
 Sequence 8, Application US/09254733
 Patent No. 6277596
 GENERAL INFORMATION:
 APPLICANT: MATANABE, MANABU
 APPLICANT: MORIYA, TATSUKI
 APPLICANT: AOKI, KAZUO
 APPLICANT: SUMIDA, NAOMI
 APPLICANT: MURAKAMI, TAKESHI
 TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBHI GENES ORIGINATING
 TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS PRODUCTION
 FILE REFERENCE: 99-0266*/1(C)(M)(C)/0014
 CURRENT APPLICATION NUMBER: US/09/254,733
 CURRENT FILING DATE: 1999-05-07
 NUMBER OF SEQ ID NOS: 52
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 8
 LENGTH: 822
 TYPE: DNA
 ORGANISM: TRICHODERMA VIRIDE MC300-1
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: (14)..(112)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (14)..(112)
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (113)..(609)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (113)..(285)
 FEATURE:
 NAME/KEY: inton
 LOCATION: (286)..(412)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (413)..(809)
 US-09-254-733-8

Query Match 19.8% Score 194.2; DB 4; Length 822;
 Best Local Similarity 69.0%; Pred. No. 80-46;
 Matches 281; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

```

QY 286 CTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 445
DB 402 CTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 461
QY 446 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 405
DB 462 TCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421

```


ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl T.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954,214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(41..723, 727..849, 853..900, 904..927)
US-08-602,657A-5

Query Match	16.88	Score	165.2	DB 2	Length	927	
Best Local Similarity	57.98	pred. No.	1-46-37				
Matches	352	Conservative	0	Mismatches	248	Indels	8
						Gaps	3

[illegible]

RESULT 12
US-09-116-622-5
; Sequence 5, Application US/09116622
; Patent No. 6080567

```

GENERAL INFORMATION:
APPLICANT: Kotof, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Christgau, Stephan S.
APPLICANT: Heide, Hansen, Hans P.
APPLICANT: Dalboeg, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: St. Joan O.
APPLICANT: Jacobson, Tina
APPLICANT: Monk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESS: No. 60805670 No. 6080570a Disk of No. 60805670h
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,622
FILING DATE: 16-July-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Artis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DRAWING NUMBER: 3954, 224-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MULTIPLE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..723, 727..849, 853..900, 904..927)
IS-09-116-622-5

```

[illegible]

Genome version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 27, 2002, 18:37:36 ; Search time 193.48 Seconds
(without alignments)
6858.790 Million cell updates/sec

Title: US-09-115-660-1

Perfect score: 983
Sequence: 1 TCGGCCGACGCTTGCAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY: 90%
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum LB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estdb:
2: em_estdb:
3: em_estdb:
4: em_estdb:
5: em_estdb:
6: em_estdb:
7: em_estdb:
8: em_estdb:
9: em_estdb:
10: em_estdb:
11: em_estdb:
12: em_estdb:
13: em_estdb:
14: em_estdb:
15: em_estdb:
16: em_estdb:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	183	18.6	720	12	AQ361561 maxb0004B
C 2	183	18.6	750	12	AQ160254 maxb0003L
C 3	182.4	18.6	583	12	AQ399120 maxb0001B
C 4	182.4	18.6	786	12	AQ325248 maxb0002M
C 5	181.6	18.5	532	10	BM134812 WHE0452.F
C 6	181	18.4	670	12	AQ447125 maxb0005C
C 7	180.8	18.4	603	12	AQ160513 maxb0006C
C 8	176.6	18.0	418	12	AQ398756 maxb0005L
C 9	164.4	15.7	753	12	AQ448084 maxb0001B
C 10	150.6	15.3	561	12	AQ396475 maxb0001M
C 11	143	14.5	490	10	BE200865 WHE0621.C
C 12	128.6	13.1	488	10	BM135798 WHE2624.C
C 13	121	12.3	646	12	AQ449078 maxb0002H
C 14	48.8	5.0	293	9	AW133010 sc13c04.Y
C 15	46.6	4.7	563	10	H132931 dt31h10.W
C 16	46.6	4.7	925	12	CNS0091P
C 17	45.6	4.6	388	9	AW103200 x043q04.X

C 18	45	4.6	492	9	A1969556
C 19	44.4	4.5	393	9	A1683810
C 20	43.6	4.4	410	9	A1513713
C 21	43.4	4.4	418	9	A1753575
C 22	43.2	4.4	463	10	BM138109
C 23	43.2	4.4	387	10	BE648949
C 24	43.2	4.4	520	10	AA911821
C 25	42.6	4.3	327	10	BM184983
C 26	42.2	4.3	225	9	AM081498
C 27	42.2	4.3	379	9	AM081507
C 28	42	4.3	455	10	BS273731
C 29	41.8	4.3	421	10	BM380099
C 30	41.6	4.2	131	9	AA252401
C 31	41.6	4.2	652	9	A1542133
C 32	41.4	4.2	240	9	A0074719
C 33	41.4	4.2	527	10	B1494147
C 34	41.4	4.2	624	9	A0091551
C 35	41.4	4.2	838	10	B1949736
C 36	41.2	4.2	386	10	B1347151
C 37	41.2	4.2	587	9	AL515343
C 38	41	4.2	240	9	A0072557
C 39	41	4.2	360	10	C68660
C 40	41	4.2	364	10	C99256
C 41	40.6	4.1	228	10	B1748403
C 42	40.6	4.1	369	9	A1289237
C 43	40.6	4.1	539	9	A1809283
C 44	40.6	4.1	561	10	B1893607
C 45	40.6	4.1	651	10	BM380055

ALIGNMENTS

RESULT 1
LOCUS AQ361561 720 bp DNA linear GSS 04-FEB-1999
DEFINITION maxb0004B19F CUGI Rice Blast BAC Library Magnaporthe oryzae genome
ACCESSION AQ361561
VERSION AQ361561.1 GI:4211400
KEYWORDS GSS.
SOURCE Magnaporthe oryzae.
ORGANISM Magnaporthe oryzae.
REFERENCE Fukuwatari T, Funai Ascomycota: Perizomycolium Sordariomycetes: Sordariomycetes: Inverticella: Magnaporthe oryzae.
AUTHORS Yu Y., Zhu H., Boyd C.A., Gaudetia H., Gayle A., Kinsbury R., Phillips K., Sasnowski M., Wang R.A. and Dean R.A.
TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe oryzae Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Jean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdc@clermson.edu
Seq primer: GGAACACGATATGATGATG
Class: BAC ends
High quality sequence stop: 421.
Location/Qualifiers
1..720
/organism="Magnaporthe oryzae"
/strain="720.15"
/db_xref="taxon:148305"
/clone="maxb0004B19F"
/clone_11b="CUGI Rice Blast BAC Library"
/tissue_type="protoplasts"
/lab_host="E. coli DH10B"
Note "vector: pBACWICH; Site_1: HindIII; Site_2: HindIII; Site_3: KpnI; Site_4: XbaI; Site_5: XbaI; Site_6: XbaI; Site_7: XbaI; Site_8: XbaI; Site_9: XbaI; Site_10: XbaI; Site_11: XbaI; Site_12: XbaI; Site_13: XbaI; Site_14: XbaI; Site_15: XbaI; Site_16: XbaI; Site_17: XbaI; Site_18: XbaI; Site_19: XbaI; Site_20: XbaI; Site_21: XbaI; Site_22: XbaI; Site_23: XbaI; Site_24: XbaI; Site_25: XbaI; Site_26: XbaI; Site_27: XbaI; Site_28: XbaI; Site_29: XbaI; Site_30: XbaI; Site_31: XbaI; Site_32: XbaI; Site_33: XbaI; Site_34: XbaI; Site_35: XbaI; Site_36: XbaI; Site_37: XbaI; Site_38: XbaI; Site_39: XbaI; Site_40: XbaI; Site_41: XbaI; Site_42: XbaI; Site_43: XbaI; Site_44: XbaI; Site_45: XbaI; Site_46: XbaI; Site_47: XbaI; Site_48: XbaI; Site_49: XbaI; Site_50: XbaI; Site_51: XbaI; Site_52: XbaI; Site_53: XbaI; Site_54: XbaI; Site_55: XbaI; Site_56: XbaI; Site_57: XbaI; Site_58: XbaI; Site_59: XbaI; Site_60: XbaI; Site_61: XbaI; Site_62: XbaI; Site_63: XbaI; Site_64: XbaI; Site_65: XbaI; Site_66: XbaI; Site_67: XbaI; Site_68: XbaI; Site_69: XbaI; Site_70: XbaI; Site_71: XbaI; Site_72: XbaI; Site_73: XbaI; Site_74: XbaI; Site_75: XbaI; Site_76: XbaI; Site_77: XbaI; Site_78: XbaI; Site_79: XbaI; Site_80: XbaI; Site_81: XbaI; Site_82: XbaI; Site_83: XbaI; Site_84: XbaI; Site_85: XbaI; Site_86: XbaI; Site_87: XbaI; Site_88: XbaI; Site_89: XbaI; Site_90: XbaI; Site_91: XbaI; Site_92: XbaI; Site_93: XbaI; Site_94: XbaI; Site_95: XbaI; Site_96: XbaI; Site_97: XbaI; Site_98: XbaI; Site_99: XbaI; Site_100: XbaI; Site_101: XbaI; Site_102: XbaI; Site_103: XbaI; Site_104: XbaI; Site_105: XbaI; Site_106: XbaI; Site_107: XbaI; Site_108: XbaI; Site_109: XbaI; Site_110: XbaI; Site_111: XbaI; Site_112: XbaI; Site_113: XbaI; Site_114: XbaI; Site_115: XbaI; Site_116: XbaI; Site_117: XbaI; Site_118: XbaI; Site_119: XbaI; Site_120: XbaI; Site_121: XbaI; Site_122: XbaI; Site_123: XbaI; Site_124: XbaI; Site_125: XbaI; Site_126: XbaI; Site_127: XbaI; Site_128: XbaI; Site_129: XbaI; Site_130: XbaI; Site_131: XbaI; Site_132: XbaI; Site_133: XbaI; Site_134: XbaI; Site_135: XbaI; Site_136: XbaI; Site_137: XbaI; Site_138: XbaI; Site_139: XbaI; Site_140: XbaI; Site_141: XbaI; Site_142: XbaI; Site_143: XbaI; Site_144: XbaI; Site_145: XbaI; Site_146: XbaI; Site_147: XbaI; Site_148: XbaI; Site_149: XbaI; Site_150: XbaI; Site_151: XbaI; Site_152: XbaI; Site_153: XbaI; Site_154: XbaI; Site_155: XbaI; Site_156: XbaI; Site_157: XbaI; Site_158: XbaI; Site_159: XbaI; Site_160: XbaI; Site_161: XbaI; Site_162: XbaI; Site_163: XbaI; Site_164: XbaI; Site_165: XbaI; Site_166: XbaI; Site_167: XbaI; Site_168: XbaI; Site_169: XbaI; Site_170: XbaI; Site_171: XbaI; Site_172: XbaI; Site_173: XbaI; Site_174: XbaI; Site_175: XbaI; Site_176: XbaI; Site_177: XbaI; Site_178: XbaI; Site_179: XbaI; Site_180: XbaI; Site_181: XbaI; Site_182: XbaI; Site_183: XbaI; Site_184: XbaI; Site_185: XbaI; Site_186: XbaI; Site_187: XbaI; Site_188: XbaI; Site_189: XbaI; Site_190: XbaI; Site_191: XbaI; Site_192: XbaI; Site_193: XbaI; Site_194: XbaI; Site_195: XbaI; Site_196: XbaI; Site_197: XbaI; Site_198: XbaI; Site_199: XbaI; Site_200: XbaI; Site_201: XbaI; Site_202: XbaI; Site_203: XbaI; Site_204: XbaI; Site_205: XbaI; Site_206: XbaI; Site_207: XbaI; Site_208: XbaI; Site_209: XbaI; Site_210: XbaI; Site_211: XbaI; Site_212: XbaI; Site_213: XbaI; Site_214: XbaI; Site_215: XbaI; Site_216: XbaI; Site_217: XbaI; Site_218: XbaI; Site_219: XbaI; Site_220: XbaI; Site_221: XbaI; Site_222: XbaI; Site_223: XbaI; Site_224: XbaI; Site_225: XbaI; Site_226: XbaI; Site_227: XbaI; Site_228: XbaI; Site_229: XbaI; Site_230: XbaI; Site_231: XbaI; Site_232: XbaI; Site_233: XbaI; Site_234: XbaI; Site_235: XbaI; Site_236: XbaI; Site_237: XbaI; Site_238: XbaI; Site_239: XbaI; Site_240: XbaI; Site_241: XbaI; Site_242: XbaI; Site_243: XbaI; Site_244: XbaI; Site_245: XbaI; Site_246: XbaI; Site_247: XbaI; Site_248: XbaI; Site_249: XbaI; Site_250: XbaI; Site_251: XbaI; Site_252: XbaI; Site_253: XbaI; Site_254: XbaI; Site_255: XbaI; Site_256: XbaI; Site_257: XbaI; Site_258: XbaI; Site_259: XbaI; Site_260: XbaI; Site_261: XbaI; Site_262: XbaI; Site_263: XbaI; Site_264: XbaI; Site_265: XbaI; Site_266: XbaI; Site_267: XbaI; Site_268: XbaI; Site_269: XbaI; Site_270: XbaI; Site_271: XbaI; Site_272: XbaI; Site_273: XbaI; Site_274: XbaI; Site_275: XbaI; Site_276: XbaI; Site_277: XbaI; Site_278: XbaI; Site_279: XbaI; Site_280: XbaI; Site_281: XbaI; Site_282: XbaI; Site_283: XbaI; Site_284: XbaI; Site_285: XbaI; Site_286: XbaI; Site_287: XbaI; Site_288: XbaI; Site_289: XbaI; Site_290: XbaI; Site_291: XbaI; Site_292: XbaI; Site_293: XbaI; Site_294: XbaI; Site_295: XbaI; Site_296: XbaI; Site_297: XbaI; Site_298: XbaI; Site_299: XbaI; Site_300: XbaI; Site_301: XbaI; Site_302: XbaI; Site_303: XbaI; Site_304: XbaI; Site_305: XbaI; Site_306: XbaI; Site_307: XbaI; Site_308: XbaI; Site_309: XbaI; Site_310: XbaI; Site_311: XbaI; Site_312: XbaI; Site_313: XbaI; Site_314: XbaI; Site_315: XbaI; Site_316: XbaI; Site_317: XbaI; Site_318: XbaI; Site_319: XbaI; Site_320: XbaI; Site_321: XbaI; Site_322: XbaI; Site_323: XbaI; Site_324: XbaI; Site_325: XbaI; Site_326: XbaI; Site_327: XbaI; Site_328: XbaI; Site_329: XbaI; Site_330: XbaI; Site_331: XbaI; Site_332: XbaI; Site_333: XbaI; Site_334: XbaI; Site_335: XbaI; Site_336: XbaI; Site_337: XbaI; Site_338: XbaI; Site_339: XbaI; Site_340: XbaI; Site_341: XbaI; Site_342: XbaI; Site_343: XbaI; Site_344: XbaI; Site_345: XbaI; Site_346: XbaI; Site_347: XbaI; Site_348: XbaI; Site_349: XbaI; Site_350: XbaI; Site_351: XbaI; Site_352: XbaI; Site_353: XbaI; Site_354: XbaI; Site_355: XbaI; Site_356: XbaI; Site_357: XbaI; Site_358: XbaI; Site_359: XbaI; Site_360: XbaI; Site_361: XbaI; Site_362: XbaI; Site_363: XbaI; Site_364: XbaI; Site_365: XbaI; Site_366: XbaI; Site_367: XbaI; Site_368: XbaI; Site_369: XbaI; Site_370: XbaI; Site_371: XbaI; Site_372: XbaI; Site_373: XbaI; Site_374: XbaI; Site_375: XbaI; Site_376: XbaI; Site_377: XbaI; Site_378: XbaI; Site_379: XbaI; Site_380: XbaI; Site_381: XbaI; Site_382: XbaI; Site_383: XbaI; Site_384: XbaI; Site_385: XbaI; Site_386: XbaI; Site_387: XbaI; Site_388: XbaI; Site_389: XbaI; Site_390: XbaI; Site_391: XbaI; Site_392: XbaI; Site_393: XbaI; Site_394: XbaI; Site_395: XbaI; Site_396: XbaI; Site_397: XbaI; Site_398: XbaI; Site_399: XbaI; Site_400: XbaI; Site_401: XbaI; Site_402: XbaI; Site_403: XbaI; Site_404: XbaI; Site_405: XbaI; Site_406: XbaI; Site_407: XbaI; Site_408: XbaI; Site_409: XbaI; Site_410: XbaI; Site_411: XbaI; Site_412: XbaI; Site_413: XbaI; Site_414: XbaI; Site_415: XbaI; Site_416: XbaI; Site_417: XbaI; Site_418: XbaI; Site_419: XbaI; Site_420: XbaI; Site_421: XbaI; Site_422: XbaI; Site_423: XbaI; Site_424: XbaI; Site_425: XbaI; Site_426: XbaI; Site_427: XbaI; Site_428: XbaI; Site_429: XbaI; Site_430: XbaI; Site_431: XbaI; Site_432: XbaI; Site_433: XbaI; Site_434: XbaI; Site_435: XbaI; Site_436: XbaI; Site_437: XbaI; Site_438: XbaI; Site_439: XbaI; Site_440: XbaI; Site_441: XbaI; Site_442: XbaI; Site_443: XbaI; Site_444: XbaI; Site_445: XbaI; Site_446: XbaI; Site_447: XbaI; Site_448: XbaI; Site_449: XbaI; Site_450: XbaI; Site_451: XbaI; Site_452: XbaI; Site_453: XbaI; Site_454: XbaI; Site_455: XbaI; Site_456: XbaI; Site_457: XbaI; Site_458: XbaI; Site_459: XbaI; Site_460: XbaI; Site_461: XbaI; Site_462: XbaI; Site_463: XbaI; Site_464: XbaI; Site_465: XbaI; Site_466: XbaI; Site_467: XbaI; Site_468: XbaI; Site_469: XbaI; Site_470: XbaI; Site_471: XbaI; Site_472: XbaI; Site_473: XbaI; Site_474: XbaI; Site_475: XbaI; Site_476: XbaI; Site_477: XbaI; Site_478: XbaI; Site_479: XbaI; Site_480: XbaI; Site_481: XbaI; Site_482: XbaI; Site_483: XbaI; Site_484: XbaI; Site_485: XbaI; Site_486: XbaI; Site_487: XbaI; Site_488: XbaI; Site_489: XbaI; Site_490: XbaI; Site_491: XbaI; Site_492: XbaI; Site_493: XbaI; Site_494: XbaI; Site_495: XbaI; Site_496: XbaI; Site_497: XbaI; Site_498: XbaI; Site_499: XbaI; Site_500: XbaI; Site_501: XbaI; Site_502: XbaI; Site_503: XbaI; Site_504: XbaI; Site_505: XbaI; Site_506: XbaI; Site_507: XbaI; Site_508: XbaI; Site_509: XbaI; Site_510: XbaI; Site_511: XbaI; Site_512: XbaI; Site_513: XbaI; Site_514: XbaI; Site_515: XbaI; Site_516: XbaI; Site_517: XbaI; Site_518: XbaI; Site_519: XbaI; Site_520: XbaI; Site_521: XbaI; Site_522: XbaI; Site_523: XbaI; Site_524: XbaI; Site_525: XbaI; Site_526: XbaI; Site_527: XbaI; Site_528: XbaI; Site_529: XbaI; Site_530: XbaI; Site_531: XbaI; Site_532: XbaI; Site_533: XbaI; Site_534: XbaI; Site_535: XbaI; Site_536: XbaI; Site_537: XbaI; Site_538: XbaI; Site_539: XbaI; Site_540: XbaI; Site_541: XbaI; Site_542: XbaI; Site_543: XbaI; Site_544: XbaI; Site_545: XbaI; Site_546: XbaI; Site_547: XbaI; Site_548: XbaI; Site_549: XbaI; Site_550: XbaI; Site_551: XbaI; Site_552: XbaI; Site_553: XbaI; Site_554: XbaI; Site_555: XbaI; Site_556: XbaI; Site_557: XbaI; Site_558: XbaI; Site_559: XbaI; Site_560: XbaI; Site_561: XbaI; Site_562: XbaI; Site_563: XbaI; Site_564: XbaI; Site_565: XbaI; Site_566: XbaI; Site_567: XbaI; Site_568: XbaI; Site_569: XbaI; Site_570: XbaI; Site_571: XbaI; Site_572: XbaI; Site_573: XbaI; Site_574: XbaI; Site_575: XbaI; Site_576: XbaI; Site_577: XbaI; Site_578: XbaI; Site_579: XbaI; Site_580: XbaI; Site_581: XbaI; Site_582: XbaI; Site_583: XbaI; Site_584: XbaI; Site_585: XbaI; Site_586: XbaI; Site_587: XbaI; Site_588: XbaI; Site_589: XbaI; Site_590: XbaI; Site_591: XbaI; Site_592: XbaI; Site_593: XbaI; Site_594: XbaI; Site_595: XbaI; Site_596: XbaI; Site_597: XbaI; Site_598: XbaI; Site_599: XbaI; Site_600: XbaI; Site_601: XbaI; Site_602: XbaI; Site_603: XbaI; Site_604: XbaI; Site_605: XbaI; Site_606: XbaI; Site_607: XbaI; Site_608: XbaI; Site_609: XbaI; Site_610: XbaI; Site_611: XbaI; Site_612: XbaI; Site_613: XbaI; Site_614: XbaI; Site_615: XbaI; Site_616: XbaI; Site_617: XbaI; Site_618: XbaI; Site_619: XbaI; Site_620: XbaI; Site_621: XbaI; Site_622: XbaI; Site_623: XbaI; Site_624: XbaI; Site_625: XbaI; Site_626: XbaI; Site_627: XbaI; Site_628: XbaI; Site_629: XbaI; Site_630: XbaI; Site_631: XbaI; Site_632: XbaI; Site_633: XbaI; Site_634: XbaI; Site_635: XbaI; Site_636: XbaI; Site_637: XbaI; Site_638: XbaI; Site_639: XbaI; Site_640: XbaI; Site_641: XbaI; Site_642: XbaI; Site_643: XbaI; Site_644: XbaI; Site_645: XbaI; Site_646: XbaI; Site_647: XbaI; Site_648: XbaI; Site_649: XbaI; Site_650: XbaI; Site_651: XbaI; Site_652: XbaI; Site_653: XbaI; Site_654: XbaI; Site_655: XbaI; Site_656: XbaI; Site_657: XbaI; Site_658: XbaI; Site_659: XbaI; Site_660: XbaI; Site_661: XbaI; Site_662: XbaI; Site_663: XbaI; Site_664: XbaI; Site_665: XbaI; Site_666: XbaI; Site_667: XbaI; Site_668: XbaI; Site_669: XbaI; Site_670: XbaI; Site_671: XbaI; Site_672: XbaI; Site_673: XbaI; Site_674: XbaI; Site_675: XbaI; Site_676: XbaI; Site_677: XbaI; Site_678: XbaI; Site_679: XbaI; Site_680: XbaI; Site_681: XbaI; Site_682: XbaI; Site_683: XbaI; Site_684: XbaI; Site_685: XbaI; Site_686: XbaI; Site_687: XbaI; Site_688: XbaI; Site_689: XbaI; Site_690: XbaI; Site_691: XbaI; Site_692: XbaI; Site_693: XbaI; Site_694: XbaI; Site_695: XbaI; Site_696: XbaI; Site_697: XbaI; Site_698: XbaI; Site_699: XbaI; Site_700: XbaI; Site_701: XbaI; Site_702: XbaI; Site_703: XbaI; Site_704: XbaI; Site_705: XbaI; Site_706: XbaI; Site_707: XbaI; Site_708: XbaI; Site_709: XbaI; Site_710: XbaI; Site_711: XbaI; Site_712: XbaI; Site_713: XbaI; Site_714: XbaI; Site_715: XbaI; Site_716: XbaI; Site_717: XbaI; Site_718: XbaI; Site_719: XbaI; Site_720: XbaI; Site_721: XbaI; Site_722: XbaI; Site_723: XbaI; Site_724: XbaI; Site_725: XbaI; Site_726: XbaI; Site_727: XbaI; Site_728: XbaI; Site_729: XbaI; Site_730: XbaI; Site_731: XbaI; Site_732: XbaI; Site_733: XbaI; Site_734: XbaI; Site_735: XbaI; Site_736: XbaI; Site_737: XbaI; Site_738: XbaI; Site_739: XbaI; Site_740: XbaI; Site_741: XbaI; Site_742: XbaI; Site_743: XbaI; Site_744: XbaI; Site_745: XbaI; Site_746: XbaI; Site_747: XbaI; Site_748: XbaI; Site_749: XbaI; Site_750: XbaI; Site_751: XbaI; Site_752: XbaI; Site_753: XbaI; Site_754: XbaI; Site_755: XbaI; Site_756: XbaI; Site_757: XbaI; Site_758: XbaI; Site_759: XbaI; Site_760: XbaI; Site_761: XbaI; Site_762: XbaI; Site_763: XbaI; Site_764: XbaI; Site_765: XbaI; Site_766: XbaI; Site_767: XbaI; Site_768: XbaI; Site_769: XbaI; Site_770: XbaI; Site_771: XbaI; Site_772: XbaI; Site_773: XbaI; Site_774: XbaI; Site_775: XbaI; Site_776: XbaI; Site_777: XbaI; Site_778: XbaI; Site_779: XbaI; Site_780: XbaI; Site_781: XbaI; Site_782: XbaI; Site_783: XbaI; Site_784: XbaI; Site_785: XbaI; Site_786: XbaI; Site_787: XbaI; Site_788: XbaI; Site_789: XbaI; Site_790: XbaI; Site_791: XbaI; Site_792: XbaI; Site_793: XbaI; Site_794: XbaI; Site_795: XbaI; Site_796: XbaI; Site_797: XbaI; Site_798: XbaI; Site_79

STIMULI: VARIOUS

Let's take "WIDE624_011_E22"
 Let's take it as "What is a unit
 library".

The issue type "Spoke"

Lab Host: (col) SOL.K

Phonostript SK; Site 1: Hook; Site 2: Xhol; 10000

with position of equilibrium. Total RNA, and poly(A) RNA were

36 and 48 hours after inoculation, a cDNA library was made

philosophical in it. Menckelhauser said at the

Pittschi, C., Vainio, C.). The cDNA library should contain

RNA preparations and DNA sequencing were performed in the

a	1688	1129	1071
---	------	------	------

14.18; Score 128.6; 103.10; Length 4335,

servative 6; Mistake 124; Models 6; Maps 2;

T T A C T A T G C T C G T G A G C A C G C T C G A C G C G G C T A C C A A A C C 211

[illegible]

Table 1

[illegible]

Abstract

[illegible]

Journal of Interpersonal Violence 38(6)

[illegible]

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

429

1000

004

4.4.1.1. INA III 1999

112241-1501 IN VIVO EFFECT OF 1,2-DICHLOROBENZENE ON THE DNA SENSITIVITY OF

01:4578215

Book 11: Signs.

Form 1: Assembly of the Solid Components

$S = \{ \langle \alpha, \beta \rangle \mid \alpha \in \mathcal{A}, \beta \in \mathcal{B} \}$

K. Sasiñewski, M. Wilfong, K. A. and Brian, R. A.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

10.000 kA

XX The present sequence is given in a specification relating to non
 CC naturally occurring xylanase activity (XA) proteins. The XA proteins
 CC comprise an amino acid sequence less than 97% identical to a naturally
 CC occurring *Bacillus circulans* xylanase. They are modified to exhibit
 CC enhanced thermostability, alkalophilicity or thermostability relative
 CC to the naturally occurring *B. circulans* xylanase. They may be used as
 CC the active compound in a bleaching agent which is used for bleaching
 CC pulp.

XX Sequence 194 AA:

Query Match 87.5% Score 1083; DB 21; Length 194;
 Best local Similarity 100.0%; Pred. No. 8,5e-95;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY 33 ITFNSRGMHGYVYVSWWSGGAQATYTNLEGGTYEISWKGMEVGRKMNPEGLNRAH 92
 |||||||
 DB 2 ttpnseqwhdyyswswsdqgqatynleqgtyelswqgqnlvqkqmpnaratn 61
 YY 93 FEVYQPNKNSYLAAYGWTRNPLVEYYIVENFGTYDPSGATDAGTVECGSTYRLGKT 152
 |||||||
 DB 62 fegvyqpqnasyayvqwttrnplveyyivenfgtydpsgatlgtvecdgsytrtqkt 121
 YY 153 RVNAPSIDGTOTPDQYWSVROKRIKSGTGTGCHPDAMRAGLNVDHYVUVAIEAYE 212
 |||||||
 DB 122 rfnapsldgtqtdqywsrvrqrkrlsgtvtgchidawaraqinvqdhyqvateayf 181
 YY 213 SSGYARITVADVG 225
 |||||||
 DB 182 ssgyaritvadvg 194

RESULT 4

AA48542
 ID AAB48542 standard; Protein: 194 AA.

AC AAB48542;

DT 05-MAR-2001 (first entry)

DE *Pseudomonas variotii* xylanase.

KW Bacterial; *Bacillus circulans*; xylanase; xylanase activity; XA;
 KM bleaching agent.

OS *Pseudomonas variotii*.

PN W0200068396-A2.

PD 16-NOV-2000.

PF 12-MAY-2000; 2000MO-US13172.

PR 12-MAY-1999; 9905-0133714.

PA (XENC-) XENCOR INC.

PI Bentzien JM;

DR WPI: 2000-679800/66.

XX Non naturally occurring XA protein with enhanced thermostability.

PT alkalophilicity or thermostability relative to the naturally occurring

XX *Bacillus circulans* xylanase is used in an agent for bleaching pulp -

PS Disclosure: Fig 16K; 114pp; English.

XX The present sequence is given in a specification relating to non

CC naturally occurring xylanase activity (XA) proteins. The XA proteins
 CC comprise an amino acid sequence less than 97% identical to a naturally
 CC occurring *B. circulans* xylanase. They are modified to exhibit
 CC enhanced thermostability, alkalophilicity or thermostability relative
 CC to the naturally occurring *B. circulans* xylanase. They may be used as
 CC the active compound in a bleaching agent which is used for bleaching
 CC pulp.

CC enhanced thermostability, alkalophilicity or thermostability relative
 CC to the naturally occurring *B. circulans* xylanase. They may be used as
 CC the active compound in a bleaching agent which is used for bleaching
 CC pulp.

SO Sequence 194 AA:

Query Match 77.9% Score 965; DB 21; Length 194;
 Best local Similarity 87.6%; Pred. No. 1.4e-83;
 Matches 169; Conservative 11; Mismatches 13; Indels 1; Gaps 0;

YY 33 ITFNSRGMHGYVYVSWWSGGAQATYTNLEGGTYEISWKGMEVGRKMNPEGLNRAH 92
 |||||||
 DB 2 ttpnseqwhdyyswswsdqgqatynleqgtyelswqgqnlvqkqmpnaratn 61
 YY 93 FEVYQPNKNSYLAAYGWTRNPLVEYYIVENFGTYDPSGATDAGTVECGSTYRLGKT 152
 |||||||
 DB 62 fegvyqpqnasyayvqwttrnplveyyivenfgtydpsgatlgtvecdgsytrtqkt 121
 YY 153 RVNAPSIDGTOTPDQYWSVROKRIKSGTGTGCHPDAMRAGLNVDHYVUVAIEAYE 212
 |||||||
 DB 122 rfnapsldgtqtdqywsrvrqrkrlsgtvtgchidawaraqinvqdhyqvateayf 181
 YY 213 SSGYARITVADVG 225
 |||||||
 DB 182 ssgyaritvadvg 194

RESULT 5

AA48548
 ID AAB48548 standard; Protein: 221 AA.

AC AAB48548;

DT 05-MAR-2001 (first entry)

DE *Cochliobolus carbonum* xylanase.

KW Bacterial; *Bacillus circulans*; xylanase; xylanase activity; XA;
 KM bleaching agent.

OS *Cochliobolus carbonum*.

PN W0200068396-A2.

PD 16-NOV-2000.

PF 12-MAY-2000; 2000MO-US13172.

PR 12-MAY-1999; 9905-0133714.

PA (XENC-) XENCOR INC.

PI Bentzien JM;

DR WPI: 2000-679800/66.

XX Non naturally occurring XA protein with enhanced thermostability.

PT alkalophilicity or thermostability relative to the naturally occurring

XX *Bacillus circulans* xylanase is used in an agent for bleaching pulp -

PS Disclosure: Fig 16Q; 114pp; English.

XX The present sequence is given in a specification relating to non

CC naturally occurring xylanase activity (XA) proteins. The XA proteins
 CC comprise an amino acid sequence less than 97% identical to a naturally
 CC occurring *Bacillus circulans* xylanase. They are modified to exhibit
 CC enhanced thermostability, alkalophilicity or thermostability relative
 CC to the naturally occurring *B. circulans* xylanase. They may be used as
 CC the active compound in a bleaching agent which is used for bleaching
 CC pulp.

XX (PRIM-) PRIMALCO LTD.
 XX
 PA Fagerstrom R, Hakola S, Jallunen I, Lantto R, Mautylae A;
 PI Paloheimo M, Siominen P, Vehmaannperae J;
 XX WPI: 1997-34168/31.
 DR N-PSDB: AAT71585.
 XX Nucleic acid encoding new xylanase(s) from Chaetomium thermophilum -
 PT useful for treating wood pulp, animal feed and flour, e.g. to
 PT facilitate bleaching
 XX
 PS Claim 1: Page 44: 76pp: English.
 XX
 CC Novel xylanases A, B and C (AAM18115-17) are encoded by the xlnA,
 CC xlnB and xlnC genes (AAT71585-87), respectively, of Chaetomium
 CC thermophilum CBS 730.95. The enzymes show optimal activity at
 CC temp. above 50 deg C and at pH 4-8 (partic. pH 5-7). They exhibit
 CC homology to family G xylanases. Xylanase A has a predicted mature
 CC protein mol. wt. of about 26 kDa. It shows 77.2% identity in 247
 CC amino acids overlap with the Chaetomium gracile xylanase H. C.
 CC thermophilum xylanases can be expressed in transformed host cells,
 CC esp. Trichoderma reesei. They are useful for enzyme-aided
 CC bleaching of wood pulp and in methods of modifying plant biomass,
 CC e.g. as a feed additive or in baking.
 CC
 XX Sequence 25] AA:
 SO

Query Match 54.8%; Score 678.5; DB 18; Length 261;
 Best local similarity 57.7%; Pred. No. 3,2e-56;
 Matches 128; Conservative 31; Mismatches 56; Indels 7; Gaps 3;

QY 1 MGGFTVALAIAAIAAGCAAFAGNATELEKROT-TPNSFGMDYVYVSWMSDGAQATV 59
 Db 1 MGGFTVALAIAAIAAGCAAFAGNATELEKROT-TPNSFGMDYVYVSWMSDGAQATV 59
 QY 60 NLEGGTYEISWEGDNIVGKGMNGLNARAIHFGYVOPNNSYLAAYGWTNPLVEY 119
 Db 56 IESGQSVTWGSGNWVQKQWMPGLDRVINYLDYPMQNSYLAVYQWIMPLIY 115
 QY 120 IVENGTITPSSGATDGLGVECDGSIYRLGKTRRNASTOTOTFQVWYKQKRISG 179
 Db 116 VESSTGTYQPSGATMSVITDGTGTYHLYTQVYMAPSLGKTYIYWSVTSKRTYQ 175
 QY 180 TVOTGCHFDAMARAGLNAGDHYVIVATPGYSSGARITV 221
 Db 176 LVEMAHINAWYQALQI-QSHDGYVATEGYSSASALVW 216

RESULT 12
 AAM60736
 ID AAM60736 standard; protein: 197 AA.
 XX

AAK60736;

02-SEP-1998 (first entry)

Xylanase A of Schizophyllum commune.

XX Family 11 xylanase; improve: thermophilicity; alkalophilicity;
 KM thermotolerance; bleach: wood pulp; processing: wheat; maize;
 KW digestibility: improving animal food additive; starch production; mutant.
 XX Schizophyllum commune.
 OS
 XX EPR28002-A2.
 PN
 XX 11-MAR-1998.
 PD
 XX 05-SEP-1997; 97EP-015412.
 PF
 XX

PR 09-SEP-1996; 96US-0709912.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 PA (NARE-) NAT RES COUNCIL.
 XX
 PI Ishikawa K, Sung WL, Yaeuchi M;
 XX WPI: 1998-161100/15
 DR
 XX Modified xylanase enzymes - useful for improving wood pulp
 PT bleaching, etc.
 PT
 XX
 PS Disclosures: Page 40; 84pp: English.
 XX
 CC AAM60728-44 represent family 11 xylanases. The specification describes a
 CC method for modifying a family 11 xylanase to improve its
 CC thermophilicity, alkalophilicity and/or thermotolerance. This method
 CC comprises modification of amino acids 10, 27 or 29 of Trichoderma reesei
 CC xylanase 11 or corresponding aligned amino acids or another family 11
 CC xylanase, replacement of one or more amino acid sequences in the
 CC N-terminal region with corresponding aligned sequences from another
 CC family 11 xylanase to form a chimeric xylanase and/or upstream extension
 CC of the N terminus by addition of upto 10 amino acids. The modified
 CC xylanases are useful for improving the bleaching of wood pulp by
 CC treatment at 55-75 degrees Celsius and pH 7.5-9.0 for 5-180 minutes. They
 CC might also be useful as digestibility-improving animal feed additives.
 CC They might also be useful in the processing of wheat or maize for starch
 CC production.
 CC
 XX Sequence 197 AA:
 SO

Query Match 53.6%; Score 664; DB 19; Length 197;
 Best local similarity 61.3%; Pred. No. 6.4e-55;
 Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

QY 34 TPNSFGMDYVYVSWMSDGAQATYTNLEGGTYEISW-GKGMNGLNARAIH 92
 Db 3 TPNSFGMDYVYVSWMSDGAQATYTNLEGGTYEISW-GKGMNGLNARAIH 92
 QY 93 FEGYVOPNNSYLAAYGWTNPLVEYIVENFGTDPSSGATDGLGVECDGSIYRLGKTR 152
 Db 63 YSGYVQPNQSYLYVQWKLSSILEYLVESYQSDPSAASHGSLTGNALYDLSIW 122
 QY 153 RVNAESTIDGTYTFQYVWSVRQDKRT---SGTYQTGCHFDAMARAGLNAGDHYVIVA 207
 Db 123 RYNAPSIDGTYQIGTWSVRNPKKAPQSISTVDVQGHIDAWKGLAMNIGSEHNYQIVA 182
 QY 208 TEGYSSGARITV 221
 Db 183 TEGYSSGARITV 196

RESULT 13
 AAB48537
 ID AAB48537 standard; protein: 197 AA.
 XX

AAB48537;

05-MAR-2001 (first entry)

Schizophyllum commune xylanase.

XX Schizophyllum commune xylanase.
 DE Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
 KW bleaching agent.
 KW
 XX Schizophyllum commune.
 OS
 XX W0200068446-A2.
 PN
 XX 16-NOV-2000.
 PD
 XX 12-MAY-2000; 2000WO-US13172.
 PF
 XX

GenCore version 4.5
Copyright (c) 1993 - 2000 Compaq Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2002, 17:28:46 ; Search time 30.85 seconds

(without alignments)
178,145 Million cell updates/sec

Title: US-09-115-660-2

Perfect score: 1238

Sequence: 1 MVEFTPVALLAALATGALAF.....VATGYPSSYARITVALWY 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

1: /cun2_5/prodata/1/1aa/56_COMB.pep:*

2: /cun2_5/prodata/1/1aa/56_COMB.pep:*

3: /cun2_5/prodata/1/1aa/56_COMB.pep:*

4: /cun2_5/prodata/1/1aa/56_COMB.pep:*

5: /cun2_5/prodata/1/1aa/56_COMB.pep:*

6: /cun2_5/prodata/1/1aa/56_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	225	2 US-08-886-765-2	Sequence 2, Appl 1
2	1238	100.0	225	4 US-09-115-660-2	Sequence 2, Appl 1
3	688.5	55.6	227	1 US-08-458-0238-4	Sequence 4, Appl 1
4	685.5	55.4	223	1 US-09-254-733-7	Sequence 7, Appl 1
5	684.5	55.3	223	4 US-08-121-4366-2	Sequence 2, Appl 1
6	678.5	54.8	261	4 US-08-768-473-2	Sequence 2, Appl 1
7	663	53.6	197	1 US-08-044-621D-29	Sequence 29, Appl 1
8	663	53.6	197	2 US-08-709-912-9	Sequence 9, Appl 1
9	663	53.6	197	2 US-09-047-370-9	Sequence 9, Appl 1
10	662.5	53.5	230	4 US-08-768-473-4	Sequence 4, Appl 1
11	636.5	51.4	190	1 US-08-044-621D-28	Sequence 28, Appl 1
12	636.5	51.4	190	1 US-08-709-912-14	Sequence 14, Appl 1
13	636.5	51.4	190	2 US-09-047-370-14	Sequence 14, Appl 1
14	635.5	51.3	190	1 US-08-044-621D-26	Sequence 26, Appl 1
15	635.5	51.3	190	1 US-08-709-912-16	Sequence 16, Appl 1
16	635.5	51.3	190	2 US-09-047-370-16	Sequence 16, Appl 1
17	634.5	51.3	190	1 US-08-044-621D-27	Sequence 27, Appl 1
18	632.5	51.1	190	1 US-08-709-912-17	Sequence 17, Appl 1
19	632.5	51.1	190	2 US-09-047-370-17	Sequence 17, Appl 1
20	628	50.7	225	1 US-08-290-929A-8	Sequence 8, Appl 1
21	588.5	47.5	226	1 US-08-507-431-6	Sequence 6, Appl 1
22	588.5	47.5	226	3 US-09-116-622-6	Sequence 6, Appl 1
23	588.5	47.5	226	4 US-09-219-277-6	Sequence 6, Appl 1
24	588.5	47.5	226	4 US-09-599-661-6	Sequence 6, Appl 1
25	586.5	47.4	241	2 US-08-902-655A-6	Sequence 6, Appl 1
26	571.5	45.2	215	1 US-08-044-621D-34	Sequence 34, Appl 1
27	568	45.1	189	1 US-08-709-912-13	Sequence 13, Appl 1

28	568	45.9	189	2 US-09-047-370-13	Sequence 13, Appl 1
29	566.5	45.8	206	1 US-08-315-695-19	Sequence 19, Appl 1
30	566	45.7	444	2 US-08-468-812-2	Sequence 2, Appl 1
31	566	45.7	344	4 US-08-590-563-2	Sequence 2, Appl 1
32	562.5	45.4	191	1 US-08-709-912-10	Sequence 10, Appl 1
33	562.5	45.4	191	2 US-09-047-370-10	Sequence 10, Appl 1
34	545.5	44.1	189	1 US-08-044-621D-34	Sequence 34, Appl 1
35	541.5	43.7	189	1 US-08-709-912-12	Sequence 12, Appl 1
36	541.5	43.7	189	2 US-09-047-370-12	Sequence 12, Appl 1
37	540	43.6	216	1 US-08-315-695-20	Sequence 20, Appl 1
38	529.5	42.8	191	1 US-08-044-621D-35	Sequence 35, Appl 1
39	529.5	42.8	200	1 US-07-744-570B-2	Sequence 2, Appl 1
40	525.5	42.4	191	1 US-08-709-912-11	Sequence 11, Appl 1
41	525.5	42.4	191	2 US-09-047-370-11	Sequence 11, Appl 1
42	506.5	40.9	278	3 US-09-260-283-2	Sequence 2, Appl 1
43	499.5	40.3	211	1 US-08-575-964-1	Sequence 1, Appl 1
44	499.5	40.3	211	2 US-08-963-500-1	Sequence 1, Appl 1
45	476	38.4	168	3 US-08-591-685-13	Sequence 13, Appl 1

ALIGNMENTS

RESULT 1
US-08-886-765-2
Sequence 2, Application US/08886765
Patent No. 5817500
GENERAL INFORMATION:
APPLICANT: Hansper, Peter Kamp
APPLICANT: Mutter, Peter
APPLICANT: Knapp, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58175000 No. 58175000disk of No. 5817500th America, Inc.
STREET: 405 Lockington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-001-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambdis, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9656
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-886-765-2

Query Match 100.0%; Score 1238; DB 2; Length 225;
Best local Similarity 100.0%; Pred. No. 2,9e-110;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MVEFTPVALLAALATGALAFPPAGNATELEKROTTPESEGMHKKYYSKMSKNAATYTN 60
|||||
1 MVEFTPVALLAALATGALAFPPAGNATELEKROTTPESEGMHKKYYSKMSKNAATYTN 60


```

TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDNESS: NO, 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: NO
ORGANISM: Trichoderma harzianum
STRAIN: Trichoderma harzianum, 20KD
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
AUTHORS: F., Tan L.U. L., Senior D.J., & Sadler
AUTHORS: J.N.
TITLE:
JOURNAL: Xylans and Xylanases
VOLUME:
ISSUE:
PAGES: 435-438
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-28

Query Match 51.4%; Score 636.5; DB 1: Length 190;
Best Local Similarity 60.7%; Pred. No. 3.7e-53;
Matches 116; Conservative 27; Mismatches 47; Indels 1; Gaps 1;

QY 32 QTPNSECWHDYVYYSWSDGGAQATYTNLEGGYELISWGDGNTVGKGMNPQINAHAI 91
DB 1 QTIIGTGYSNYYYSWMDGHAGVTYTNCGGSPYVMSNSNGTVGKGMNPQINAHAI 60

QY 92 HFEQVYQNGNSYLAAYGWTNPNVEYTVENFGTYDPSNGTIDLGTECNSTYRKKT 151
DB 61 NFGSYNPNNGNSYLSYSGSRNPLEYIVENFGTYNPGTGATKLGTEVLSGVSVDIYRI 120

QY 152 TRVNAFSLIIGIQTFFQYMSVRFQIKRTSGTVJGCHFDAMARALNVNTHHYVQIVATGAY 211
DB 121 QRVNPSIIGIATFFQYMSVRFQIKRTSGTVJGCHFDAMARALNVNTHHYVQIVATGAY 179

QY 212 FSSGYARITVA 222
DB 180 FSSGSASTIVS 190

```

```

STATE: New York
COUNTRY: USA
ZIP: 10172 0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsson M.T., Warren F.
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2482
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M.
AUTHORS: Roy, C.
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F.
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Sadler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
US-08-709-912-14

Query Match 51.4%; Score 636.5; DB 1: Length 190;
Best Local Similarity 60.7%; Pred. No. 3.7e-53;
Matches 116; Conservative 27; Mismatches 47; Indels 1; Gaps 1;

QY 32 QTPNSECWHDYVYYSWSDGGAQATYTNLEGGYELISWGDGNTVGKGMNPQINAHAI 91
DB 1 QTIIGTGYSNYYYSWMDGHAGVTYTNCGGSPYVMSNSNGTVGKGMNPQINAHAI 60

QY 92 HFEQVYQNGNSYLAAYGWTNPNVEYTVENFGTYDPSNGTIDLGTECNSTYRKKT 151
DB 61 NFGSYNPNNGNSYLSYSGSRNPLEYIVENFGTYNPGTGATKLGTEVLSGVSVDIYRI 120

QY 152 TRVNAFSLIIGIQTFFQYMSVRFQIKRTSGTVJGCHFDAMARALNVNTHHYVQIVATGAY 211
DB 121 QRVNPSIIGIATFFQYMSVRFQIKRTSGTVJGCHFDAMARALNVNTHHYVQIVATGAY 179

QY 212 FSSGYARITVA 222
DB 180 FSSGSASTIVS 190

```

```

RESULT 12
US-08-709-912-14
Sequence 14, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung D.C., Wang L.
APPLICANT: Yaguchi M., Makoto
APPLICANT: Ishikawa M., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESS: Fitzpatrick, Celia, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York

```

```

RESULT 13
US-09-047-370-14
Sequence 14, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung D.C., Wang L.
APPLICANT: Yaguchi M., Makoto

```


FILED DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-26

Query Match 51.38: Score 635.5: DB 1: Length 190:
Best Local Similarity 60.28: Pred. No. 4.6e-53:
Matches 115: Conservative 28: Mismatches 47: Indels 1: Gaps 1:

QY 32 QTTNSKGMHAGYYSWMSDGAQATYTNLEGGTYELSMWCGNLVGRKGMNPLNARAI 91
DB 1 OTTPTGTGYNNGYFYSWNMGHGVYTTNGCTGDP SYWMSNSNGNFVGGKGMWGTNKKVI 60
QY 92 HFGCVYQPNNSYLAAYGWTNPLVEVYIVENFGTYDPSGATDICTVCTGNSYRRAKI 151
DB 61 NFSGVNPNNSYLAAYGWSKRNPLIEVYIVENFGTYDPSGATDICTVCTGNSYRRAKI 120
QY 152 TRVAPSLTGTTFDYWWSYQDKRTSGTGTGTHLAKARAGIANNKHYVQIVALEKY 211
DB 121 QRVNOPSITGATFYQWWSVRNRHSSSVNTANHFNAWQDGLTL-GRMUYQIVAVEKY 179
QY 212 FSSGVARITVA 222
DB 180 FSSGSASITVS 190

RESULT 15
US-08-709-912-16
Sequence 16, Application US/08709912
Patent No. 5759840

GENERAL INFORMATION:
APPLICANT: Sana Dr., Wing L
APPLICANT: Yajuchi Dr., Makoto
TITLE OF INVENTION: Modification of Xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Colla, Harper, and Schinto
STREET: 277 Park Ave.
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPILED: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912

FILING DATE: 09 SEP-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Olson Mr, Warren E

REGISTRATION NUMBER: 27290
REFERENCE/MARKET NUMBER: 1039, 2000

TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:

LENGTH: 190 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal
ORIGINAL SOURCE:

ORGANISM: Trichoderma reesei
STRAIN: xyn 11

PUBLICATION INFORMATION:
AUTHORS: Tortorene, A

AUTHORS: Mach, R. L.

AUTHORS: Messner, R

AUTHORS: Gonzalez, R

AUTHORS: Kalkkinen, N

AUTHORS: Harkki, A

AUTHORS: Kubicek, C. P.

JOURNAL: Biotechnology

VOLUME: 10

PAGES: 1461-1465

DATE: 1992

US-08-709-912-16

Query Match 51.38: Score 635.5: DB 1: Length 190:
Best Local Similarity 60.28: Pred. No. 4.6e-53:
Matches 115: Conservative 28: Mismatches 47: Indels 1: Gaps 1:
QY 32 QTTNSKGMHAGYYSWMSDGAQATYTNLEGGTYELSMWCGNLVGRKGMNPLNARAI 91
DB 1 OTTPTGTGYNNGYFYSWNMGHGVYTTNGCTGDP SYWMSNSNGNFVGGKGMWGTNKKVI 60
QY 92 HFGCVYQPNNSYLAAYGWTNPLVEVYIVENFGTYDPSGATDICTVCTGNSYRRAKI 151
DB 61 NFSGVNPNNSYLAAYGWSKRNPLIEVYIVENFGTYDPSGATDICTVCTGNSYRRAKI 120
QY 152 TRVAPSLTGTTFDYWWSYQDKRTSGTGTGTHLAKARAGIANNKHYVQIVALEKY 211
DB 121 QRVNOPSITGATFYQWWSVRNRHSSSVNTANHFNAWQDGLTL-GRMUYQIVAVEKY 179
QY 212 FSSGVARITVA 222
DB 180 FSSGSASITVS 190

Search completed: April 27, 2002, 18:36:26
Job time: 4060 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2002, 18:33:56 ; Search time 52.22 seconds

(without alignments)
414,020 Million cell updates/sec

Title: US-09-115-660-2

Perfect score: 12.8

Sequence: 1 MGGTPVALALATGALAF.....VAIEGYFSSGYARITVAWG 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 28438 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 28438

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR,71:*

1: piri:*

2: piri:*

3: piri:*

4: piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	691.5	55.9	219	2	S71472 endo-1,4-beta-xyla
2	689.5	55.7	227	2	S43919 endo-1,4-beta-xyla
3	689	55.7	241	2	S71473 endo-1,4-beta-xyla
4	684.5	55.3	223	2	S39883 endo-1,4-beta-xyla
5	680.5	55.0	225	1	S57477 endo-1,4-beta-xyla
6	667	53.6	222	2	S39154 xylanase 1 - funu
7	663	53.6	197	1	A44597 endo-1,4-beta-xyla
8	659	53.2	232	2	JC7577 endo-1,4-beta-xyla
9	637.5	51.5	221	1	S57469 endo-1,4-beta-xyla
10	636.5	51.4	190	1	A44593 endo-1,4-beta-xyla
11	636.5	51.4	190	1	A44595 endo-1,4-beta-xyla
12	634.5	51.3	190	1	A44594 endo-1,4-beta-xyla
13	599.5	48.4	221	2	JC7107 endo-1,4-beta-xyla
14	585.5	47.3	335	2	T50601 endo-1,4-beta-xyla
15	573	46.3	343	1	J50500 endo-1,4-beta-xyla
16	554.5	44.8	241	2	T37005 endo-1,4-beta-xyla
17	553	44.7	240	1	S47512 endo-1,4-beta-xyla
18	540	43.6	240	1	J50591 endo-1,4-beta-xyla
19	529	42.7	644	1	I40712 endo-1,4-beta-xyla
20	528	42.6	661	1	S59633 endo-1,4-beta-xyla
21	505.5	40.8	210	2	C83762 endo-1,4-beta-xyla
22	498	40.2	656	1	S59631 endo-1,4-beta-xyla
23	470.5	38.0	213	1	I40569 endo-1,4-beta-xyla
24	469.5	37.9	213	1	S48126 endo-1,4-beta-xyla
25	468.5	37.8	213	1	S01734 endo-1,4-beta-xyla
26	452	36.5	354	1	S51779 endo-1,4-beta-xyla
27	427	34.5	261	1	J01935 endo-1,4-beta-xyla
28	400	32.3	261	1	S12745 endo-1,4-beta-xyla
29	397.5	32.1	228	1	WMBXP endo-1,4-beta-xyla

30	390	31.5	211	2	S49542 endo-1,4-beta-xyla
31	389.5	31.5	789	2	S58235 endo-1,4-beta-xyla
32	388	31.3	211	1	JC1198 endo-1,4-beta-xyla
33	385	31.1	211	1	S48229 endo-1,4-beta-xyla
34	372	30.0	229	2	S39155 xylanase 2 - funu
35	371	30.0	954	1	S20907 endo-1,4-beta-xyla
36	365	29.5	781	2	S51592 Xyln precursor - R
37	356	28.8	209	2	JC4909 endo-1,4-beta-xyla
38	355.5	28.7	802	2	A36910 xylanase, beta(1,3
39	299.5	24.2	607	2	S49528 endoxylanase - fun
40	296	24.9	607	2	S24754 endo-1,4-beta-xyla
41	248	20.0	608	2	S51295 xylanase (EC 3.2.1
42	240.5	19.4	266	1	S48865 endo-1,4-beta-xyla
43	145	11.7	50	2	A61149 endo-1,4-beta-xyla
44	115	9.3	2817	2	H97033 uncharacterized pr
45	113	9.1	40	2	P02022 endo-1,4-beta-xyla

ALIGNMENTS

RESULT 1
S71472
endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile
N:Alternate names: xylanase A
C:Species: Chaetomium gracile
C>Date: 09-Dec-1997 #sequence _revision 09-Dec-1997 #text_change 20-Jun-2000
R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
Curr. Genet. 29, 73-80, 1995
A>Title: Two family G xylanase genes from Chaetomium gracile and their expression in
A:Reference number: S71472; MIMD:96118924
A:Accession: S71472
A:Molecule type: DNA
A:Residues: 1-219 <YOS>
A:Cross-references: EMBL:D49850; NID:q139857; PIDD:AA08649.1; PIDD:q144858
A:Accession: S78206
A:Molecule type: protein
A:Residues: 31-45;82-94;152-160 <YOH>
C:Genetics:
C:Function: 81/2
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-30/Domain: signal sequence #status predicted <SIO>
F:31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F:42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
F:115;206/Active site: Glu #status predicted

Query Match 55.9%; Score 691.5; DB 2; Length 219;
Best local Similarity 59.1%; Pred. No. 1.2e+47;
Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps 5;
Y 1 MGGTPVALALATGALAFPAAGNAT---ELEKQCTPNSGHHKQYYSWMSKAGQAI 57
DB 1 MVSERKAL---LLDAGALAEFP NVTQMLVARAGTPSGTGNNQPVSPFWTNGQIVN 56
Y 58 YTNLEGTTELSKDDGNNLVGGKGNPGLNARMIHEGQYQPPNGSNVLAAYEATNPVE 117
DB 57 YUNGAGSISVQWQNCNFGGKGNPGLA-ARTINSGTFSPGNGSLAYGQNPINLVE 115
Y 118 YVIVENGTFDPSSGADLATEVEDGSIYELKRTTNAPSIHGICFEDYGVSVHDKRT 177
DB 116 YVIVESGTYDPSQASKFETIOODGSTYTIKATTRYNQSIHGISTFQKFWSVKHNS 175
Y 178 SGTVQVGHDPDANARAGLVNGBHYQIVATEYFSSGYARITVA 222
DB 176 SGGVNAVAAHFNMAQGLKLGSHNYQIVATEYFSSGSSNITS 219
RESULT 2

Db 121 YIVENGTGTHPDAARAGIANNVNDHVVQIVATGEGYFSSGVARITVA 222
 179 GTVGTGTHPDAARAGIANNVNDHVVQIVATGEGYFSSGVARITVA 222
 Db 181 GSVNTANHRNMAAGUGLTL-GTMDYQIVAVKGFSSGSSASTIVS 223

RESULT 5

S57477

endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - *Emmericella nidulans*

N-Alternate names: xylanase 1

C:Species: *Emmericella nidulans*, *Aspergillus nidulans*

C:Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 23-Mar-2001

C:Accession: S57477

R:Peres-Gonzalez, J.A.

submitted to the EMBL Data Library, June 1995

A:Description: Expression in *Saccharomyces cerevisiae* of two xylanase encoding genes from

A:Reference number: S57469

A:Accession: S57477

A:Molecule type: DNA

A:Residues: 1-225 <PER>

A:Cross-references: EMBL:Z49892; NID:q870832; PDB:CAA90074.1; PDB:q870833

C:Genetics:

A:Insertions: 93/2

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xyloridic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta xylanase; endo-1,4-beta-xylanase homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:1-19/Domain: signal sequence #status predicted <Sig>

F:20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>

F:48-225/Domain: endo-1,4-beta-xylanase homology <XLY>

F:121-212/Active site: Glu #status predicted

Query Match 55.0% Score 680.5; DB 1: Length 225;

Best Local Similarity 56.0% Pred. No. 9,3e-47;

Matches 129; Conservative 31; Mismatches 57; Indels 11; Gaps 4;

Db 1 MGCTPVALLAATGALAPAG--NATELEKROTTPNSEGHDDYYSSWMSDGG 53
 1 MVSFSTSLAASPSPASRPAARVSVAVKRTIIOPTGNNKRYFSSYNNAGHGGYTY 59
 Oy 54 AQAATYNNLEGGTYFISMGDCNNLVGKGNPGLNARA1HEGGYOPNGNSYLAAYGTFN 113
 59 GDVYITNGAGGSYTYQSNVNGNFVGKGNPGL-STRITNGSGFSPSGNGYLAAYGTFN 117
 Db 114 PLVEYIVVENGTGTHPDAARAGIANNVNDHVVQIVATGEGYFSSGVARITVA 173
 118 PLVEYIVVENGTGTHPDAARAGIANNVNDHVVQIVATGEGYFSSGVARITVA 177
 Oy 174 DKRTSGTGTGTHPDAARAGIANNVNDHVVQIVATGEGYFSSGVARITVA 221
 178 SKRTSGTGTGTHPDAARAGIANNVNDHVVQIVATGEGYFSSGVARITVA 224

RESULT 6

S39154

xylanase 1 - fungus (*Trichoderma reesei*)

C:Species: *Trichoderma reesei*

C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999

C:Accession: S39154

R:Teeterloren, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkbrenner, N.; Harkki, A.; Kuhl

Biochemistry 10, 1461-1465, 1992

A:Title: The two major xylanases from *Trichoderma reesei*: characterization of both enzymes

A:Reference number: S39154

A:Accession: S39154

A:Molecule type: DNA

A:Residues: 1-222 <TOES>

A:Cross-references: EMBL:X69573; NID:q396563; PDB:GMA49293.1; PDB:q396564

C:Genetics:

A:Gene: xyl1
 A:Insertions: 90/2
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 F:44-222/Domain: endo-1,4-beta-xylanase homology <XLY>

Query Match 53.9% Score 667; DB 2: Length 222;
 Best Local Similarity 57.1% Pred. No. 1.1e-45;
 Matches 128; Conservative 32; Mismatches 60; Indels 4; Gaps 4;

Db 1 MGCTPVALLAATGALAPAG--NATELEKROTTPNSEGHDDYYSSWMSDGGATY 58
 1 MVSFSTSLAASPSPASRPAARVSVAVKRTIIOPTGNNKRYFSSYNNAGHGGYTY 59
 Oy 59 TNEGTYEISMGDCNNLVGKGNPGLNARA1HEGGYOPNGNSYLAAYGTFN:VEY 118
 60 TNEGTYEISMGDCNNLVGKGNPGLNARA1HEGGYOPNGNSYLAAYGTFN:VEY 119
 Db 119 YIVENGTGTHPDAARAGIANNVNDHVVQIVATGEGYFSSGVARITVA 173
 120 YIVENGTGTHPDAARAGIANNVNDHVVQIVATGEGYFSSGVARITVA 179
 Oy 179 GTVGTGTHPDAARAGIANNVNDHVVQIVATGEGYFSSGVARITVA 222
 180 GSVNTANHRNMAAGUGLTL-GTMDYQIVAVKGFSSGSSASTIVS 222

RESULT 7

A44597

endo-1,4-beta-xylanase (EC 3.2.1.8) A - bracket fungus (*Schizophyllum commune*)

N-Alternate names: xylanase A

C:Species: *Schizophyllum commune*

C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 06-Dec-1996

C:Accession: A44597; S41411; A05147; S38973

R:Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A:Reference number: A44597

A:Accession: A44597

A:Molecule type: protein

A:Residues: 1-197 <YAG>

A:Experimental source: strain Delmar ATCC 38948

R:Bray, M.R.; Clarke, A.J.

Eur. J. Biochem. 219, 821-827, 1994

A:Title: Identification of a glutamate residue at the active site of xylanase A from

A:Reference number: S41411; M01D:94155888

A:Accession: S41411

A:Status: preliminary

A:Molecule type: protein

A:Residues: 83-123

R:Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Campbell, K.; Yaguchi, M.; Durask,

FEBS Lett. 334, 296-300, 1993

A:Title: Amino acid sequence and the thermostability of xylanase A from *Schizophyllum* spp

A:Reference number: S38973; M01D:94061044

A:Accession: S38973

A:Molecule type: protein

A:Residues: 1-197 <OKU>

A:Experimental source: ATCC 48548

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xyloridic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F:12-197/Domain: endo-1,4-beta-xylanase homology <XLY>

F:87-184/Active site: Glu #status predicted

F:111-160/Disulfide bonds: #status experimental

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2002, 18:36:31 / Search time 31.77 seconds

(without alignments)
274.218 Million cell updates/sec

Title: US-09-115-660-2

Perfect score: 1218

Sequence: 1 MWGTPVALAAIATGALAF.....VATECYSSVAKITVALWG 225

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1248	100.0	225	1 XYNL_THELA	043097; thermomyces
2	806.5	65.1	221	1 XYNL_GORCA	006662; coellobolus
3	689.5	55.7	227	1 XYNL_HUMIN	P55344; humicola in
4	680.5	55.0	225	1 XYNL_EMENT	P55342; emeticella
5	667	53.9	222	1 XYNL_TRIRE	P36217; trichoderma
6	663	53.6	197	1 XYNL_SCHCO	P36809; schizophyll
7	660	53.3	233	1 XYNL_MAGOR	P55335; magnaporthe
8	637.5	51.5	221	1 XYNL_EMENT	P55343; emeticella
9	632	51.1	225	1 XYNL_ASAPK	P48824; aspergillus
10	631	51.0	225	1 XYNL_ASAPG	P55340; aspergillus
11	630.5	50.9	190	1 XYNL_TRIHA	P48793; trichoderma
12	587.5	47.5	335	1 XYNL_STRLI	P26675; streptomyces
13	540	43.6	240	1 XYNL_SIRLI	P26220; streptomyces
14	529	42.7	644	1 XYNL_CELFI	P54965; cellulomonas
15	474	38.2	210	1 XYNL_BACST	P18479; bacillus st
16	470.5	38.0	213	1 XYNL_BACST	P18479; bacillus st
17	468.5	37.8	213	1 XYNL_BACST	P18479; bacillus st
18	427	34.5	512	1 XYNL_CLOSJ	P34558; clostridium
19	409	32.3	261	1 XYNL_CLOSA	P17137; clostridium
20	406.5	32.0	228	1 XYNL_BACPO	P00634; bacillus pu
21	390	31.5	211	1 XYNL_ASITU	P55331; aspergillus
22	388	31.3	211	1 XYNL_ASAPK	P48824; aspergillus
23	387	31.1	211	1 XYNL_ASAPG	P55340; aspergillus
24	385	31.1	211	1 XYNL_ASAPW	P55342; aspergillus
25	372	30.0	229	1 XYNL_TRIRE	P36217; trichoderma
26	371	30.0	954	1 XYNL_KUMEL	P29126; ruminovoccu
27	355.5	28.7	802	1 XYNL_RUMEL	P29126; ruminovoccu
28	296	23.9	607	1 XYNL_NECOP	P29127; neocallimast
29	251.5	20.3	625	1 XYNL_PIRSP	P12667; pirumyces s
30	248	20.0	608	1 XYNL_PIRSP	P12667; pirumyces s
31	106	8.6	772	1 VPA_KOTHA	P36407; bovine rota
32	104.5	8.4	398	1 CARA_KHINI	P00370; thricops vi
33	102.5	8.3	1286	1 ALDA_PECOL	P00370; thricops vi

34	100	8.1	772	1 VPA_KOTHA	P36408; bovine rota
35	98.5	8.0	433	1 FASC_XENLA	Q91837; xenopus fac
36	94	7.6	433	1 SHII_ECOLI	P09750; escherichia
37	94	7.6	1080	1 MLI5_GAEEL	Q23356; carnosobadi
38	94	7.6	2710	1 TOXA_CICOL	P16154; clostridium
39	93	7.5	474	1 SHII_ECOLI	P09745; escherichia
40	93	7.5	492	1 FSCI_MOUSE	Q61553; mus musculu
41	92	7.4	366	1 OMJA_RHILV	Q05811; rhizobium 1
42	92	7.4	772	1 VPA_KOTHA	Q09113; human rotav
43	92	7.4	4303	1 PRDI_HUMAN	P98163; human sapin
44	91.5	7.4	976	1 AMY_RHIF1	P30269; poliovirus p
45	91	7.4	323	1 PEMP_PENIA	P00796; penicillium

ALIGNMENTS

RESULT	ID	Sequence	Standard	PRT	AA
1	XYNL_THELA	STANDARD	PRT	225	AA
AC	043097				
DT	15-DEC-1998 (Rel. 37, created)				
DT	15-DEC-1998 (Rel. 37, last sequence update)				
DT	15-JUN-1999 (Rel. 38, last annotation update)				
DE	Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan xylanohydrolase).				
DE	XYNL				
GN	XYNA				
OS	Thermomyces lanuginosus (Humicola lanuginosa).				
OC	Eukaryota; Fungi; Ascomycota; mitospore Ascomycota; Thermomyces.				
OX	NCBI_TaxID=5541				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=DSM 5826 / TSIKLINSKY				
RX	MEDLINE=97033440; PubMed=8879171				
RA	Schlaecher A., Holzmann K., Hayn M., Steiner W., Schwab H.				
RT	X-ray structure and modeling studies.				
RL	Biochemistry 37:13475-13485(1998).				
CC	-1- FUNCTION: THERMOSTABLE XYLANASE.				
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xyans.				
CC	-1- PATHWAY: XYLAN DEGRADATION.				
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).				
CC	This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb.ch/announc/ or send an email to license@isb.slb.ch).				
CC	EMBL: 035436; AAB94633.1				
CC	PDB: 1YNA; 12-EBH-97				
CC	InterPro: IPR001147; Glyco_hydro_11				
CC	PIRAT: PF00457; Glyco_hydro_11; 1				
CC	PRINTS: PR00911; GLYHYDRLASE11				
CC	PROSITE: PS00776; GLYCOSYL_HYDROL_11.1; 1				
CC	PROSITE: PS00777; GLYCOSYL_HYDROL_11.2; 1				
CC	XYNL degradation: glycolase; glycosidase; signal; 4D structure.				
CC	SIGNAL				
CC	CHAIN				
CC	ACT_SITE				
CC	117	117			
CC	ENDO 1,4-BETA-XYLANASE				
CC	NOTLEPROFILE				

This SWISS PROF entry is copyright - it is produced through a collaboration between The Swiss Institute of Bioinformatics and the EMBL consortium. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb.sib.ch/announcements> or send an email to licensing@sib.ch).

This SWISS-PHOT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL consortium. The European Bioinformatics Institute, there are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb.sib.ch/announcements> or send an email to license@isb.sib.ch).

EMBL: X76047; CAA53632.1; -
 DR HSPD: Q43997; 1YNA.
 DR InterPro: IP001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; hydrolase; glycosidase; signal.
 KW Xylan degradation; hydrolase; glycosidase; signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 227 ENDO-1,4-BETA-XYLANASE 1.
 FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 227 AA; 25601 MW; 502FF6ADCEADALF CRG64;

Query Match 55.7%; Score 689.5; DB 1; Length 227;
 Best Local Similarity 55.8%; Pred. No. 9, 8a-50;
 Matches 126; Conservative 41; Mismatches 62; Indels 7; Gaps 3;

DB 1 MVSFTPAALAAATCAALAA...PPAGNATELEKRRQTTPNSGMDHGYYSWSGGCAQ 55
 11 MSLKSLVLAATVASSIAAPDEVPDNDSTALQAKQVTENAMHNGFYYSWSGGCAQ 60

DB 56 AATTNIEGSGIYELISWIGKGLVSGKGNKGLNKAHFEVGYOPKNSYLAAYGWTENP 115
 61 VQNTLEGSRVGVWRNTGNEVGGKGNKPG-TGRTINYGVPNPGNGLAYGWTENP 119

DB 116 VEYVIEVNEGIVPSSGATLGTVECDGSIYRLKTRVAPSLDSTQIFGQVSWKQK 175
 120 VEYVIEVNEGIVPSSGATLGTVECDGSIYRLKTRVAPSLDSTQIFGQVSWKQK 179

DB 176 RSTSTVGTGCHPDAWAKAGLVNNDHYQVATRGVSSVARTV 221
 180 RAGGSVMQNHFNAMQCHMPL-GQHYGVVATEGVSSGSESLIYV 224

DB 180 RAGGSVMQNHFNAMQCHMPL-GQHYGVVATEGVSSGSESLIYV 224

RESULT 4
 XYN1_EMENT STANDARD; PRT: 225 AA.
 ID XYN1_EMENT STANDARD; PRT: 225 AA.
 AC P55332; Q00173;
 DT 01-OCT-1996 (Rel. 14, created)
 DT 01-OCT-1996 (Rel. 14, last sequence update)
 DT 01-NOV-1997 (Rel. 15, last annotation update)
 DE Endo-1,4-beta-xylinase 1 precursor (EC 3.2.1.8) (Xylanase 1)
 OS (1,4-beta-D-xylan xylanohydrolase 1).
 DE Emeritella nidulans (Aspergillus nidulans).
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiales; Trichocomaceae; Emmentella.
 CC NCBI_TaxID=5072;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96246210; PubMed=8787417;
 RA Perez-Gonzalez J.A., de Graaf L.H., Visser J., Karon D.;
 RT "Molecular cloning and expression in *Saccharomyces cerevisiae* of two
 RT Aspergillus nidulans xylanase genes.";
 RL Appl. Environ. Microbiol. 62:2179-2182(1996).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylan to
 CC linkages in xylans.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC
 CC This SWISS-Prot entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed, usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb.slb.ch).
 CC
 DR EMBL: Z49892; CAA90074.1; -
 DR HSPD: P48793; 1XND.
 DR InterPro: IP001177; Glyco_hydro_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; hydrolase; glycosidase; signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 225 ENDO-1,4-BETA-XYLANASE 1.
 FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 225 AA; 24070 MW; 670F2C79602C7FEC CRG64;

Query Match 55.0%; Score 680.5; DB 1; Length 225;
 Best Local Similarity 56.6%; Pred. No. 5, 3a-4%;
 Matches 129; Conservative 41; Mismatches 57; Indels 11; Gaps 4;

DB 1 MVSFTPAALAAATCAALAA...PPAGNATELEKRRQTTPNSGMDHGYYSWSGGCAQ 55
 11 MSLKSLVLAATVASSIAAPDEVPDNDSTALQAKQVTENAMHNGFYYSWSGGCAQ 60

DB 54 AATTNIEGSGIYELISWIGKGLVSGKGNKGLNKAHFEVGYOPKNSYLAAYGWTENP 114
 59 GQVITNMGAGSYTYQWNSVNGVPGSKGNKPG-SIRIINYGSPNPNNSYLAAYGWTENP 117

DB 114 PLVEYVIEVNEGIVPSSGATLGTVECDGSIYRLKTRVAPSLDSTQIFGQVSWKQK 173
 118 PLVEYVIEVNEGIVPSSGATLGTVECDGSIYRLKTRVAPSLDSTQIFGQVSWKQK 177

DB 174 RSTSTVGTGCHPDAWAKAGLVNNDHYQVATRGVSSVARTV 221
 178 RSTSTVGTGCHPDAWAKAGLVNNDHYQVATRGVSSVARTV 224

DB 178 RSTSTVGTGCHPDAWAKAGLVNNDHYQVATRGVSSVARTV 224

RESULT 5
 XYN2_TRIE STANDARD; PRT: 222 AA.
 ID XYN2_TRIE STANDARD; PRT: 222 AA.
 AC P56217;
 DT 01-JUN-1994 (Rel. 29, created)
 DT 01-JUN-1994 (Rel. 29, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE Endo-1,4-beta-xylinase 2 precursor (EC 3.2.1.8) (Xylanase 2)
 OS (1,4-beta-D-xylan xylanohydrolase 2).
 GN XYN2.
 OS Trichoderma reesei (Hypocrea jecorina).
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocryales; Hypocryaceae; Hypocrea.
 CC NCBI_TaxID=51453;
 RN 11
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=C30;
 RX MEDLINE=93103679; PubMed=169024;
 RA Toivonen A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.;
 RT "The two major xylanases from *Trichoderma reesei*: characterization of
 RT both enzymes and genes.";
 RL Biotechnology 10:1461-1465(1992).
 CC [2]
 RN 12
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RC STRAIN=C30;
 RX MEDLINE=94283373; PubMed=8013449;
 RA Toivonen A., Harkki A., Rouvinen J.;
 RT "Three-dimensional structure of endo-1,4-beta-xylinase 1 from
 RT *Trichoderma reesei*: two conformational states in the active site.";
 RL EMBL J. 13:2494-2501(1994).
 CC [3]
 RN 13
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RC STRAIN=C30;
 RX MEDLINE=95127653; PubMed=7827044;
 RA Toivonen A., Rouvinen J.;
 RT "Structural comparison of two major endo 1,4-xylinases from
 RT *Trichoderma reesei*.";
 KL Biochemistry 34:847-856(1995).
 RN 14

[illegible]

QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Dib	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Dib	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	1	2	3	4	5																																																																																															

01 01-JUN-1994 (rel. 29, last sequence update)
02 15-DEC-1998 (rel. 47, last annotation update)
03 Entry 1.4 beta xylanase A (EC 3.2.1.8) (Xylanase A) (1,4 beta-D-xylan
04 xylanoylhydrolase A).
05 Schizophyllium commune (bracket fungus).
06 Schizophyllum commune (bracket fungus).
07 Enzyme A. Enzyme. Brachymeria: Hymenoptera: Homobasidiomycetes;
08 Stereum: Schizophyllaceae; Schizophyllium.
09 NCBI Taxid 5434.
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
00
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
00
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
00
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
00
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
00
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
00
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
00
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
00
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
00
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
8

DB 183 FEIYSSGATITV 196

RESULT 7

XYN2_MAGGR STANDARD: PRT: 213 AA.

AC P55335: Q01171:

DI 01-OCT-1996 (Rel. 34, Created)

DI 01-OCT-1996 (Rel. 34, Last sequence update)

DI 10-MAY-2000 (Rel. 39, Last annotation update)

DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)

DE (1,4-beta-D-xylan xylanohydrolase 22).

OS Magnaporthe oryzae (Rice blast fungus) (Pyricularia grisea).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe;

OX NCBI_TaxID:148405;

KN 111

RP SEQUENCE FROM N.A.

RC MEDLINE:96172742; PubMed:8589407;

RA Wu S.C., Kautman S., Darvill A.G., Albersheim P.

RT "Purification, cloning and characterization of two xylanases from

Magaporthe oryzae, the rice blast fungus."

RL Mol. Plant Microbe Interact. 8:506-514(1995).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

linkages in xylans.

CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL

HYDROLASES).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL institution.

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL: 147529; AAC41683.1;

DR HSSP: 043097; LYNA.

DR InterPro: IP800117; Glyco_hydro_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PRINTS: PR00911; GLYHYDRLASE1.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KM Xylan degradation; Hydrolyase; Glycosidase; Signal.

FT SIGNAL 1 39 POTENTIAL.

FT CHAIN 40 233 ENDO-1,4-BETA-XYLANASE 22.

FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).

FT ACT_SITE 217 217 PROTON DONOR (BY SIMILARITY).

SO SEQUENCE 233 AA; 25491 MW; 40096383658198 CRC64;

Query Match 53.3%; Score 660; DB 1; Length 233;

Best local Similarity 53.7%; Pred. No. 2,6e-47;

Matches 144; Conservative 36; Mismatches 59; Indels 12; Gaps 6;

DB 1 MVSFTVALALAAATG:ALAPPA--GNAT-----ELEKROTPNSKCHMHTYYSSNMSSOG 52

DB 1 MVSFTSLVIVVALAGSALAIFAPDCKMTCHPEQIMRKROSTPSSTRHNGYYSSMTWDS 60

DB 53 GAQATYINLEGGYEISWGDGKGNVGGKGNPGLNAAHIFEGYVGP--MNSVLAECW 110

DB 61 ASPOVGVNNGNSYSVOMQSGNFGVGGKGNP--GSKSTIYSSTFN--VNNCNAATVLYCW 119

DB 111 TRNPLVEVYIVENFGYDPSSGATDGLTVECDSTYRLGKTTFRVNAVSLGGLQITFWYWS 170

DB 120 TQNPILVEYIIVENGFEVNPQNSASRGTLDAGCTYILHESFRVNGSLKQIRIFQGYMA 179

DB 171 VRODKRTSGTVGTGCHFDAMARAGLNVNGCHYQIVAFIEYSSGVARITV 221

DB 180 IROKRNKSGIVNTGCFQAMERAGMGM GHHNYIVATEGYMSAQNINIV 229

RESULT 8

XYN2_EMBL1 STANDARD: PRT: 221 AA.

AC P55335: Q00176:

DI 01-OCT-1996 (Rel. 34, Created)

DI 01-OCT-1996 (Rel. 34, Last sequence update)

DI 01-NOV-1997 (Rel. 35, Last annotation update)

DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)

DE (1,4-beta-D-xylan xylanohydrolase 2).

OS Aspergillus nidulans (Aspergillus nidulans).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiomycetes; Trichocomaceae; Eurotiales.

OX NCBI_TaxID:5072;

KN 111

RP SEQUENCE FROM N.A.

RC MEDLINE:96286210; PubMed:8787417;

RA Perez-Gonzalez J.A., de Graaf L.H., Visser J., Raman D.

RT "Molecular cloning and expression in Saccharomyces cerevisiae of two

Aspergillus nidulans xylanase genes."

RL Appl. Environ. Microbiol. 62:2179-2182(1996).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

linkages in xylans.

CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL

HYDROLASES).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL institution.

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL: 249893; CAA0074.1;

DR HSSP: 048793; LXND.

DR InterPro: IP800117; Glyco_hydro_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PRINTS: PR00911; GLYHYDRLASE1.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KM Xylan degradation; Hydrolyase; Glycosidase; Signal.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 221 ENDO-1,4-BETA-XYLANASE 2.

FT ACT_SITE 117 117 NUCLEOPHILE (BY SIMILARITY).

FT ACT_SITE 208 208 PROTON DONOR (BY SIMILARITY).

SO SEQUENCE 221 AA; 23517 MW; 42665800DE9475 CRC64;

Query Match 51.5%; Score 637.5; DB 1; Length 221;

Best local Similarity 54.0%; Pred. No. 1.7e-45;

Matches 122; Conservative 36; Mismatches 59; Indels 9; Gaps 4;

DB 1 MVSFTVALALAAATG:ALAPPA--GNAT-----ELEKROTPNSKCHMHTYYSSNMSSOG 56

DB 1 MVSFTSLVIVVALAGSALAIFAPDCKMTCHPEQIMRKROSTPSSTRHNGYYSSMTWDS 57

DB 57 TYNLEGGYEISWGDGKGNVGGKGNPGLNAAHIFEGYVGP--MNSVLAECW 110

DB 58 TYNLEGGYEISWGDGKGNVGGKGNPGLNAAHIFEGYVGP--MNSVLAECW 110

DB 117 EYIVENFGYDPSSGATDGLTVECDSTYRLGKTTFRVNAVSLGGLQITFWYWS 170

DB 117 EYIVENFGYDPSSGATDGLTVECDSTYRLGKTTFRVNAVSLGGLQITFWYWS 170

DB 177 TSGSVITQNHFIAMSGDGLT--GTHNYQIVAVVGYGSSNSASTIVS 221

RESULT 9
XNBN ASPAK STANDARD: PRF: 225 AA.
AC P48794.
DT 01 FEB 1996 (rel. 44, created)
DT 01 FEB 1996 (rel. 44, last sequence update)
DT 15 JUL 1999 (rel. 48, last annotation update)
DE beta-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
DN XNBN.
OS Aspergillus fumigatus (var. kawachii).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocommataceae; mitosporic Trichocommataceae; Aspergillius.
OX NCBI_TaxID: 50617.
BN 111
RP SEQUENCE FROM N.A.
RC STRAIN: 190 4066.
RA To K.
RT 1.
SC Submitted (SEP 1994) to the EMBL/Genbank/DBJ databases.
CC 1. CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylan to
hydroxy-xylooligosaccharides.
CC 2. SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
HYDROLASES).
CC This SwissProt entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb.slb.ch/annouce/>
or send an email to license@isb.slb.ch).
CC
CC EMBL: D38070; J04024; X17.
CC BSSP: P09850; X17.
CC InterPro: IPR001147; glyco_hydro_11.
CC Pfam: PF00457; glyco_hydro_11_1.
CC PRINITS: PR00911; GLYHYDASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation: hydrolyses glycosidase: signal.
CC STANAL: 1 18
CC ACT SITE 19 225
CC ACT SITE 121 121
CC ACT SITE 212 212
CC PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 225 AA: 24146 MW: 5481408 Da pI 5.715 cI 6.42
Query Match 51.0% Score 6.42; ID: 1; Length 225
Best Local Similarity 54.4% Pred. No. 45
Matches 119; Conserved 42; Mismatches 60; Indels 8; Gaps 4;
UY 9 LAALAAATGALAPVATNATE-----LEK--KQTENSRSEMHGGYYSWMSGCAATYTNLE 62
DB 8 LCFAAAKAAVAVPDSVAVRSDALIMLSRSTPSSTGKNGYYSWMTGQIVTYTNIN 67
UY 63 GATVEIEMWAGNIGVGGKGMNINARALHEGCVYQPNNSYLAAYGQINLVYVIVE 122
DB 68 AGAVYVEMSNVGNVGGKGMNINARALHEGCVYQPNNSYLAAYGQINLVYVIVE 126
UY 124 NGATVPSGATGATVEVDSYVRLKRTKYNALSHKQVDFDYVSWVGRKRTSTVQ 182
DB 127 SYGVNPNSSGATGYKTVSDSVYDLYATPRNASTLGATATGYWVGRKNGVGTIV 186
UY 184 TGTHTAMARAGLNVNLDHYVQVATVEGYSSTYARIV 221
DB 187 TSNHFNAMAKLGMNLTGHNYQVATVEGYSSGSSSTIV 224

RESULT 11
XNBN ASPAK STANDARD: PRF: 190 AA.
AC P48794.
DT 01 FEB 1996 (rel. 44, created)
DT 01 FEB 1996 (rel. 44, last sequence update)
DT 15 DEC 1998 (rel. 47, last annotation update)
DE beta-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
DN XNBN.
OS Aspergillus fumigatus (var. kawachii).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocommataceae; mitosporic Trichocommataceae; Aspergillius.
OX NCBI_TaxID: 50617.
BN 111
RP SEQUENCE FROM N.A.
RC STRAIN: 190 4066.
RA To K.
RT 1.
SC Submitted (SEP 1994) to the EMBL/Genbank/DBJ databases.
CC 1. CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylan to
hydroxy-xylooligosaccharides.
CC 2. SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
HYDROLASES).
CC This SwissProt entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb.slb.ch/annouce/>
or send an email to license@isb.slb.ch).
CC
CC EMBL: D38070; J04024; X17.
CC BSSP: P09850; X17.
CC InterPro: IPR001147; glyco_hydro_11.
CC Pfam: PF00457; glyco_hydro_11_1.
CC PRINITS: PR00911; GLYHYDASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation: hydrolyses glycosidase: signal.
CC STANAL: 1 18
CC ACT SITE 19 225
CC ACT SITE 121 121
CC ACT SITE 212 212
CC PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 225 AA: 24057 MW: 5481408 Da pI 5.715 cI 6.42
Query Match 51.0% Score 6.42; ID: 1; Length 225
Best Local Similarity 54.4% Pred. No. 45
Matches 119; Conserved 42; Mismatches 60; Indels 8; Gaps 4;
UY 9 LAALAAATGALAPVATNATE-----ACNATLEKRTTPNSRMHGGYYSWMSGCAATYTNLE 62
DB 8 LCFAAAKAAVAVPDSVAVRSDALIMLSRSTPSSTGKNGYYSWMTGQIVTYTNIN 67
UY 63 GATVEIEMWAGNIGVGGKGMNINARALHEGCVYQPNNSYLAAYGQINLVYVIVE 122
DB 68 AGAVYVEMSNVGNVGGKGMNINARALHEGCVYQPNNSYLAAYGQINLVYVIVE 126
UY 124 NGATVPSGATGATVEVDSYVRLKRTKYNALSHKQVDFDYVSWVGRKRTSTVQ 182
DB 127 SYGVNPNSSGATGYKTVSDSVYDLYATPRNASTLGATATGYWVGRKNGVGTIV 186
UY 184 TGTHTAMARAGLNVNLDHYVQVATVEGYSSTYARIV 221
DB 187 TSNHFNAMAKLGMNLTGHNYQVATVEGYSSGSSSTIV 224

DB 71 NMSSPOLYSTSWNTGTFNFAKRWANF-GKRFVQYSTSPNSGNALALVDMISNVEY 129
 QY 119 YIVENITLTHSSATLITLVTITLSTLVLKKTETVENALSLIKTLPDQVSWVPOURKS 178
 DB 119 YIVENITLTHSSATLITLVTITLSTLVLKKTETVENALSLIKTLPDQVSWVPOURKS 178
 DB 140 YIVENITLTHSSATLITLVTITLSTLVLKKTETVENALSLIKTLPDQVSWVPOURKS 187
 QY 179 GIVQVITHEFAWAGLINVGNHRYVQIVATETPSSGARTVAWG 225
 DB 188 GIVQVITHEFAWAGLINVGNHRYVQIVATETPSSGARTVAWG 244
 RESULT 13
 XYNM_SIRCL STANDARD PRG 240 AA
 ID XYNM_SIRCL STANDARD PRG 240 AA
 AC P26220;
 DT 01 MAY 1992 (rel. 22, last sequence update)
 DT 01 MAY 1992 (rel. 22, last sequence update)
 DT 15 JUL 1999 (rel. 48, last annotation update)
 DE Rodo 1,4 beta-xylanase precursor (p3.2.1.8) (Xylanase C)
 DE (1,4 beta-D-xylan xylanhydrolase C)
 EN XLANC
 CC Streptomyces lividans.
 CC Bacteria: Firmicutes; Actinobacteria; Actinobacteridae; Streptomyces
 CC Actinomycetales; Streptomyces; Streptomycesaceae; Streptomyces
 CC NCBI TaxID 1916;
 CC 111
 CC SEQUENCE FROM N.A. AND SEQUENCE OF 50-80.
 CC STRAIN 65 / 1426;
 CC MEDLINE 94074749; PubMed 174421;
 CC Shaheen P., Roy C., Yanoichi M., Morosoff R., Kluepfel D.,
 CC "Sequences of three genes specifying xylanases in Streptomyces
 CC lividans."
 CC Gene 107176.82(1991).
 CC FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE MAJOR
 CC COMPONENT OF PLANT CELL-WALLS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylanidic
 CC linkages in xylans.
 CC 1 PATHWAY: XLAN DEGRADATION.
 CC 1 SUBCELLULAR LOCATION: Secreted.
 CC 1 SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC This SWISS prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
 CC The European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/announcements/](http://www.isb-sib.ch/announcements)
 CC or send an email to license@isb-sib.ch).
 CC EMBL: M64553; AAA26836.1;
 CC EMBL: A254073; CAA01708.1;
 CC PIR: J80591.1; J80591.
 CC HSSP: P09850; 1XNB.
 CC InterPro: IPR001187; glyco_hydro_11.
 CC Pfam: PF00457; glyco_hydro_11;
 CC PRINTS: PR00911; GLYDRLASE1.
 CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1;
 CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2;
 CC K0 Kylan degradation; Hydrolase; Glycosidase; Signal;
 CC FT SIGNAL 1 49
 CC FT CHAIN 1 490 EMBL 1,4-BETA-XYLANASE D.
 CC FT ACT SITE 144 144 NUCLEOPHILE (BY SIMILARITY).
 CC FT ACT SITE 226 226 PROTON DONOR (BY SIMILARITY).
 CC SEQUENCE 240 AA; 25673 MW; K56644157H01427A C6064;
 QY Query Match 44.6%; Score 5409; DB 13; Length 240;
 Post local similarity 50.9%; Pred. No. 1; Re 37;
 Matches 110; Conserved Eve. 26; Mismatches 66; Indels 14; Gaps 5;
 11 ALAALVALAP ANATLEKRLTPNSRMHRYVYSWSSGCAQATVIMLEATVE 68

DB 34 ALAVALSLITPQIAVAATITLNGT - - - - -DEMYSEFWITDQGSMTINDGYSI 87
 QY 69 SNGRSENVGKGMWGNARALDEFEVYQNGNSYLAAYGEMFNIVVEYVSEPTYP 129
 DB 69 SNGRSENVGKGMWGNARALDEFEVYQNGNSYLAAYGEMFNIVVEYVSEPTYP 129
 DB 88 GEMVGNVAKWMSG - - - - -DNVRYMFTNIVGNVYGLYMSINLVEYIVNMSYR 145
 QY 129 PSSNPLATVETSLVLAETKTRVANSSTHRTQTPQVSWVQURK 186
 DB 129 PSSNPLATVETSLVLAETKTRVANSSTHRTQTPQVSWVQURK 186
 DB 146 FL - GYGVYSSSGKIDYDTOTRYNMSVSKRTFGQVSWVQSKVLSNGIITGNI 204
 QY 187 FLAARAGLINVGNHRYVQIVATETPSSGARTVA 222
 DB 204 FLAARAGLINVGNHRYVQIVATETPSSGARTVA 249
 RESULT 14
 XYNM_SIRCL STANDARD PRG 644 AA
 ID XYNM_SIRCL STANDARD PRG 644 AA
 AC P54865;
 DT 01 OCT 1996 (rel. 34, first update)
 DT 01 OCT 1996 (rel. 34, last sequence update)
 DT 15 OCT 2001 (rel. 40, last annotation update)
 DE Rodo 1,4 beta-xylanase D precursor (p3.2.1.8) (Xylanase D) (XYIID).
 EN XYNM.
 CC Cellulomonas flint.
 CC Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Micrococcales; Cellulomonadaceae; Cellulomonas.
 CC NCBI TaxID 1708;
 CC 111
 CC SEQUENCE FROM N.A.
 CC STRAIN 221;
 CC MEDLINE 94224156; PubMed 8170499;
 CC Millward Sadler S.J., Poole D.M., Benlissat B., Hazlewood G.P.,
 CC Clarke J.H., Gilbert R.J.,
 CC "Evidence for a general role for high-affinity non-catalytic
 CC cellulose binding domains in microbial plant cell wall hydrolases."
 CC Mol. Microbiol. 11:375-382(1994).
 CC FUNCTION: ENDOACTING XYLANASE WHICH DISPLAYS NO DEPENDABLE
 CC ACTIVITY AGAINST POLYSACCHARIDES OTHER THAN XLAN. HYDROLYSES
 CC GLYCOSIDIC BONDS WITH RETENTION OF ANEMERIC CONFIGURATION.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylanidic
 CC linkages in xylans.
 CC 1 PATHWAY: XLAN DEGRADATION.
 CC 1 SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC This SWISS prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC The European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcements/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL: X76729; CAA54145.1;
 CC HSSP: P09850; 1XNB.
 CC InterPro: IPR001919; CHO_2.
 CC InterPro: IPR001187; glyco_hydro_11.
 CC InterPro: IPR002509; Polysac-deacet.
 CC Pfam: PF00554; CHO_2;
 CC Pfam: PF00457; glyco_hydro_11;
 CC Pfam: PF01522; Polysac-deacet_1;
 CC PRINTS: PR00911; GLYDRLASE1.
 CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1;
 CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2;
 CC K0 Hydrolase; Glycosidase; Signal; Repeat;
 CC FT SIGNAL 1 44
 CC FT CHAIN 44 644 EMBL 1,4-BETA-XYLANASE D.
 CC FT DOMAIN 44 240 CATALYTIC.
 CC FT DOMAIN 241 245 LINKER ("HUNG") (GLY RICH BOX).
 CC FT DOMAIN 246 644 2 X BB AA APPROXIMATE CHO-LIKE REPEATS.
 CC REPEAT 246 444 1.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: April 27, 2002, 18:35:51 ; Search time 74.8 seconds

(Without alignments)
520.372 Million cell updates/sec

Title: US-09-115-660-2

Perfect score: 1238

Sequence: 1 MGCFFPVALMIALMIALGALF.....VATIEYFSSGYAKIIVAVWG 225

Scoring table: BLASTSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mure: *
8: SP organelle: *
9: SP plant: *
10: SP rodent: *
11: SP virus: *
12: SP vertebrate: *
13: SP unclassified: *
14: SP virus: *
15: SP bacteriap: *
16: SP archaeap: *
17: SP archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	965	77.9	194	P81536	Paecilomyces
2	821.5	66.4	227	G90V23	G90V23 helminthosp
3	785	63.4	295	G9C1R2	G9C1R2 fusarium ox
4	775.5	62.6	227	G00283	G00283 ascochyta p
5	716.5	57.9	231	G14447	G14447 cochlidiobol
6	701.5	56.7	231	G00350	G00350 cochlidiobol
7	692.5	55.9	227	G9HCE1	G9HCE1 humicola ut
8	691.5	55.9	219	G12579	G12579 chaetomium
9	689	55.7	241	G12580	G12580 chaetomium
10	684.5	55.3	223	G00284	G00284 trichoderma
11	676.5	54.6	231	G9C1R1	G9C1R1 fusarium ox
12	671.5	54.2	224	G99015	G99015 trichoderma
13	660.5	53.4	221	P87037	P87037 aspergillus
14	659	53.2	232	G9HFA4	G9HFA4 aspergillus
15	638	51.5	290	G9HEZ0	G9HEZ0 phanerocha
16	638	51.5	290	G9HEY9	G9HEY9 phanerocha

17	632.5	51.1	223	G90VP9	G90VP9 trichoderma
18	610.5	49.4	223	G9HPH0	G9HPH0 penicillium
19	599.5	48.4	221	G90J02	G90J02 penicillium
20	585.5	47.3	335	G9RKN6	G9RKN6 streptomyces
21	579	46.8	283	G96UV7	G96UV7 penicillium
22	573	46.3	228	G95962	G95962 streptomyces
23	573	46.3	338	G96265	G96265 thecamos
24	563	45.5	335	G9R0M4	G9R0M4 streptomyces
25	562.5	45.4	335	G9ROBH	G9ROBH cellulomonas
26	562.5	45.4	335	G008346	G008346 streptomyces
27	561	45.3	329	G9RKH9	G9RKH9 streptomyces
28	557.5	44.8	191	G9EBM9	G9EBM9 streptomyces
29	554.5	44.8	241	G9R172	G9R172 streptomyces
30	553	44.7	240	G96013	G96013 streptomyces
31	541	43.7	240	G94716	G94716 claviceps p
32	528	42.6	661	G959674	G959674 pseudomonas
33	517.5	41.8	129	G92245	G92245 marasmius
34	505.5	40.8	210	G9KEP3	G9KEP3 bacillus ba
35	498	40.2	656	G94300	G94300 cellulosic
36	481.5	38.9	211	G94993	G94993 acetomans p
37	474	38.3	461	G952375	G952375 candida
38	470.5	38.0	213	G959254	G959254 bacillus su
39	470.5	38.0	217	G992402	G992402 phanerocha
40	469.5	37.9	213	G959256	G959256 bacillus sp
41	467.5	37.8	213	G92B36	G92B36 bacillus sp
42	462	37.4	212	G95989	G95989 penicillium
43	452	36.5	354	G9R094	G9R094 bacillus sf
44	452	36.5	354	G959257	G959257 bacillus sp
45	448.5	36.2	120	G90W04	G90W04 ascochyta p

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	194 AA.
AC	P81536			
DT	01-JUN-2000 (TREMUR)	14, Created		
DT	01-JUN-2000 (TREMUR)	14, Last sequence update		
DT	01-JUN-2000 (TREMUR)	17, Last annotation update		
DE	ENDO-1,4-BETA-XYLANASE (EC 4.2.1.8) (XYLANASE) (1,4-BETA-D			
DE	XYLAN XYLANOXYDOLASE) (DX) (FRAGMENT).			
OS	Paecilomyces variotii.			
OC	Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiomycetes; Trichothomycetes; mitosporic Trichothomycetes; Paecilomyces.			
OX	NCBI_TaxID=45996;			
RN	[1]			
RP	X-RAY CRYSTALLOGRAPHY (1.59 ANGSTROMS), AND PARTIAL SEQUENCE.			
RC	SERAIN-BALINIER;			
RX	MEDLINE=20060955; PubMed=10623548;			
RA	Kumar P.R., Eswarasanthi S., Vithayathil P.J., Viswanatha M.A.,			
RT	"The tertiary structure at 1.59 A resolution and the proposed amino			
RT	acid sequence of a family-11 xylanase from the thermophilic fungus			
RT	Paecilomyces variotii bantier."			
RL	J. Mol. Biol. 295:581-593(2000).			
CC	- CATALYTIC ACTIVITY: ENDHYDROLYSIS OF 1,4-BETA-D XYLANS.			
CC	- LINKAGES IN XYLANS.			
CC	- PATHWAY: XYLAN DEGRADATION.			
CC	- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL			
CC	HYDROLASES).			
CC	HYDROLASES).			
DR	HSSP: 043097; IYNA.			
DR	InterPro: IPR001147; Glyco_hydro_11.			
DR	Prima: PR00457; Glyco_hydro_11; 1.			
DR	PRINIS: PR00911; GLYHYDROLASE11.			
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F11_1; 1.			
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
KW	Xylan degradation; Hydrolase; Glycosidase; Acetylation.			
FT	MOD_RES	1		
FT	MOD_RES	1		
FT	ACT_SITE	86	86	ACETYLATION
FT	ACT_SITE	178	178	NUCLEOPHILE (BY SIMILARITY).
FT	ACT_SITE	178	178	PROTON DONOR (BY SIMILARITY).
FT	DISULFID	110	154	

10	Q02244;	PRELIMINARY;	FT:	223 AA.
AC	Q02244;			
DI	01-NOV-1996 (ITEMBRL: 01, Created)			
DT	01-NOV-1996 (ITEMBRL: 01, Last sequence update)			
DI	01-JUN-2001 (ITEMBRL: 17, Last annotation update)			
DE	ENOXALANASE 11.			
GN	XLN2.			
OS	Trichoderma reesei (Hypocrea jecorina).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocerales; Hypocercaceae; Hypocrea.			
OX	NCBI_TaxID=51451;			
PN	11			
RP	SEQUENCE FROM N.A.			
RA	MF01.NE=94088442; PubMed 8264524;			
RA	Saarelainen R., Palonen M., Fagerstrom R., Suominen P.L.,			
RA	Nevalainen K.M.;			
RT	"Cloning, sequencing and enhanced expression of the Trichoderma reesei			
RT	enoxalase 11 (p 9) gene xln2."			
RL	Mol. Gen. Genet. 241:497-504(1993).			
DE	EMBL: S67387; AAB29346.1; "			
DE	HSSP: P36217; IXYO.			
DR	InterPro: IPR001137; glyco_hydro_11.			
DR	Pfam: PF00457; glyco_hydro_11; 1.			
DR	PRINTS: PR009111; GLEHYDRLASE11.			
DR	PROSITE: PS00776; GLYCOSYL-HYDROL_F11.1; 1.			
DR	PROSITE: PS00777; GLYCOSYL-HYDROL_F11.2; 1.			
KW	Xylan degradation; Hydrolyase; Glycosidase.			
NO	SEQUENCE: 223 AA; 24069 MW; 79668149EADA22F9 CnR64;			

Query Match	55.38;	Score 684.5;	DB 3;	Length 224;
Fast Local Similarity	57.18;	Pred. No. 4.3e-45;		
Matches 126;	Conservative 32;	Mismatches 61;	Indels 3;	Gaps 2

[illegible]

RESULT	11
CGCRL1	
ID	CGCRL1
AC	CGCRL1
DT	01-JUN-2001 (FEMBLrel. 17, created)
DT	01-JUN-2001 (FEMBLrel. 17, last sequence update)
DT	01-JEC-2001 (FEMBLrel. 19, last annotation update)
DE	XYLANASE 4 PROTEIN
CN	XYLA
OS	Fusarium oxysporum f. sp. lycopersici.
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC	Hypocreales; Mitosporic Hypocreales; Fusarium.
OX	NCBI_TaxID 59765;
RN	111
RP	SEQUENCE FROM N.A.
RA	Herra C., Gomez-Gomez E., Romero M.;
RT	"Cloning and characterization of two family 11 xylanase genes in
RT	Fusarium oxysporum f. sp. lycopersici."
RL	Submitted (MAR 2000) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF246841; MAK27975.1;
DR	HSSP; 041097; LYNA.
DR	InterPro; IPR001137; Glyco_hydro_11.

DR PRINTS: PR00911; GLHYDLASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
SQ SEQUENCE 231 AA; 25638 MW; 94D2C6C6B890792 CRC64

Query Match:	54.68;	Score 676.5;	DB 3;	Length 281;
Best Local Similarity	56.58;	Pred. No. 1.8e-44;		
Matches 130;	Conservative 29;	Mismatches 60;	Indels 11;	Gaps 4

QY	1	MYGFTPLVALAALAAIGALAF-----ACAGAT-LERKQIPLNSRGMHGGVYSWMSD	1
Db	1	MYSEKSLIAASALGALAAHPFDELDFOHDSNSTSVLPAPQVQNSRQYENGGVYSWMSD	60
QY	52	GGAAATTTNLEAGTVELSKMDSQNLVQKGMNPGCNAAVHFEESVYQIMNSTLAVYQMI	1
Db	61	GGGAAATKMGTCSEHYQVQVQNMKNSEFVGGKGMNPG-TGRIIMVSGEFSQNMVYQVGM	1
QY	112	HNPLVEVYIVENIGTQVPSGSGATDLDGTVEKDSYRIKQKTRVMAVSLETHQVPEQVSW	17
Db	120	KSPVLEVYVLESQTYNPSASQDQKQTVNDDQTDIALQVTRVQVPSLDSDQVFNLMVAI	17
QY	172	RODRKTSQTVLYRHPDAAARAKIINQNDHVVQVIAATVNSYSSGAVARIYV	221
Db	180	RNRKTSQVAMQVTFMANSASQMKI-QGHVYQVLIATKQVSSQSSSTIYV	228

RESUL 12
U99015

AD	Q99015:	PRELIMINARY:	PT:	223 AA.
DE	01-NOV-1996 (JEMBL:01, (created)			
DT	01-NOV-1996 (JEMBL:01, last sequence update)			
DT	01-JUN-2001 (JEMBL:01, 17, last annotation update)			
DE	HYA-XYLANASE, PRECOURSOR.			
GN	XYN2.			
OS	<i>Trichoderma reesei</i> (Hypocetia feculina).			
OC	Eucaryotes; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocetiales; Hypocetaceae; Hypocetia.			
KN	NCBI_TaxID=51451;			
RX	11)			
RP	SEQUENCE FROM N.A.			
RX	STRAIN QM 6A:			
RX	MEDLINE: 97076932; PubMed 8975597;			
RA	La Grange D.C., Piotrowski J.S., van Zyl W.H.:			
RT	"Expression of a trichoderma reesei beta-xylanase gene (XYN2) in			
RL	<i>Saccharomyces cerevisiae</i> ."			
RT	Appl. Environ. Microbiol. 62:1036-1044(1996).			
DR	EMBL: 024191; AA050278.1); -			
DR	HSSP: P36217; IXYO.			
DR	InterPro: IPR001137; Glyco_hydro_11.			
DR	PIfam: PF00457; Glyco_hydro_11; 1.			
DR	PRIN1S: PR00911; GUHYBLASE11.			
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
KW	Signal: xylan degradation; hydrolase; Glycosidase.			
FT	SIGNAL			
FT	CHAIN	1	33	POTENTIAL.
FT	CHAIN	34	223	HYA-XYLANASE.
SO	SEQUENCE	223 AA:	23981 MW:	F096F55D0690EBA C0664:

[illegible]


```

Db      1  MVSFNLTVAVSAATCALAPPEFHNGIHVEPROSTPAIGTNNCEVSPWIKAGSVTV 60
QY      59  INLEGTVELSMGIGGONLWCKGKMPALNARALHFEQVYQPNNGSYLAAYGWTRNPLVEY 118
Db      61  NNCPADGYSVITWNNADNFVAGKQWNG-SAGALSTANQPNNGSYLSVYQWSTNPLVEY 119
QY      119  YIVENFGTYDPSGATDIACTVEEDGS1YRIQKTRVNADPSIRCTQIFDOYWSYKDKRIS 178
Db      120  YILEDFGTVMFAVSLHKGITLSDGATYEDYEGIRVNEPSTQGTATPNQYWSLESSKRSS 179
QY      179  GTVOTGCHITAMAKGLINWGRHYQIVATECTFESSGATATVAIWG 225
Db      180  GTVITAMHFAWKQLGILPL-GTFNYQIVATEGYOSSGSSIVTVNPAW 225

```

Search completed: April 27, 2002, 18:43:58
 Job time: 487 sec

